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OM protein - protein search, using sw model
Run on:       January 28, 2007, 17:28:16 ; Search time 217 Seconds
                                           (without alignments)
                                           1348.486 Million cell updates/sec

Title:        US-10-677-669-69 ·
Perfect score: 3135
Sequence:     1 MCSRVPLLPLLLLLALGPG..........PLMGFPGPGLQSPLHAKPYI 598
Scoring table: BLOSUM62
Searched:     2782304 seqs, 48933398 residues
Total number of hits satisfying chosen parameters:     2782304
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
              Maximum Match 100%
              Listing first 1500 summaries
Database :    A_Geneseq_200701:*
              1: geneseqp1980s:*
              2: geneseqp1990s:*
              3: geneseqp2000s:*
              4: geneseqp2001s:*
              5: geneseqp2002s:*
              6: geneseqp2003as:*
              7: geneseqp2003bs:*
              8: geneseqp2004s:*
              11: geneseqp2007s:*
    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.
                                SUMMARIES

No.   Score  Match Length DB  ID                    Description
RESULT 1
ID   AAY06484 standard; protein; 598 AA.
DE   Human tumour-associated protein PRO357.
PN   WO9935170-A2.
PD   15-JUL-1999.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;    Score 3135;  DB 2;  Length 598;
     Best Local Similarity  100.0%;    Pred. No. 4.3e-190;
RESULT 2
ID   AAB01322 standard; protein; 598 AA.
DE   Human PRO357 polypeptide.
PN   WO200032776-A2.
PD   08-JUN-2000.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;    Score 3135;  DB 3;  Length 598;
     Best Local Similarity  100.0%;    Pred. No. 4.3e-190;
RESULT 3
ID   AAY93691 standard; protein; 598 AA.
DE   Amino acid sequence of novel polypeptide PRO357.
PN   WO200037640-A2.
PD   29-JUN-2000.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;    Score 3135;  DB 3;  Length 598;
     Best Local Similarity  100.0%;    Pred. No. 4.3e-190;
RESULT 4
ID   AAU83643 standard; protein; 598 AA.
DE   Human PRO protein, Seq ID No 104.
PN   WO200208288-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;    Score 3135;  DB 5;  Length 598;
     Best Local Similarity . 100.0%;    Pred. No. 4.3e-190;
RESULT 5
ID   ADY31844 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   WO200193983-A1.
PD   13-DEC-2001.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;    Score 3135;  DB 5;  Length 598;
     Best Local Similarity  100.0%;    Pred. No. 4.3e-190;
RESULT 6
ID   ABU55931 standard; protein; 598 AA.
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DE   Human secreted/transmembrane protein PRO357.
PN   US200214959-A1.
PD   03-OCT-2002.
PA   (GETH) GENENTECH INC.
     Query Match        100.0%;    Score 3135;  DB 6;  Length 598;
     Best Local Similarity  100.0%;    Pred. No. 4.3e-190;
RESULT 7
ID   ABU80790 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003036635-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;    Score 3135;  DB 6;  Length 598;
     Best Local Similarity  100.0%;    Pred. No. 4.3e-190;
RESULT 8
ID   ABO33756 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003045687-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;    Score 3135;  DB 6;  Length 598;
     Best Local Similarity  100.0%;    Pred. No. 4.3e-190;
RESULT 9
ID   ABU60241 standard; protein; 598 AA.
DE   Human PRO polypeptide #12.
PN   US2002132768-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;    Score 3135;  DB 6;  Length 598;
     Best Local Similarity  100.0%;    Pred. No. 4.3e-190;
RESULT 10
ID   ABU64927 standard; protein; 598 AA.
DE   Human secreted/transmembrane protein PRO357.
PN   US2002173463-A1.
PD   21-NOV-2002.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;    Score 3135;  DB 6;  Length 598;
     Best Local Similarity  100.0%;    Pred. No. 4.3e-190;
RESULT 11
ID   ABU58361 standard; protein; 598 AA.
DE   Novel human secreted protein PRO357.
PN   US2002150976-A1.
PD   17-OCT-2002.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;    Score 3135;  DB 6;  Length 598;
     Best Local Similarity  100.0%;    Pred. No. 4.3e-190;
RESULT 12
ID   ABU57247 standard; protein; 598 AA.
DE   Human PRO357 protein.
PN   US2002142958-A1.
PD   03-OCT-2002.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;    Score 3135;  DB 6;  Length 598;
     Best Local Similarity  100.0%;    Pred. No. 4.3e-190;
RESULT 13
ID   ABU56312 standard; protein; 598 AA.
DE   Human secreted/transmembrane protein, PRO357.
PN   US2002132981-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;    Score 3135;  DB 6;  Length 598;
     Best Local Similarity  100.0%;    Pred. No. 4.3e-190;
RESULT 14
ID   ABU60352 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2002168715-A1.
PD   14-NOV-2002.
PA   (GETH ) GENENTECH INC.
     Query Match        100.0%;    Score 3135;  DB 6;  Length 598;
     Best Local Similarity  100.0%;    Pred. No. 4.3e-190;
RESULT 15
ID   ABU82099 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
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PN   US2003088063-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 16
ID   ABU11313 standard; protein; 598 AA.
DE   Human pro357 protein sequence.
PN   US2002127643-A1.
PD   12-SEP-2002.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 17
ID   ABU67132 standard; protein; 598 AA.
DE   Human PRO polypeptide #12.
PN   US2002165143-A1.
PD   07-NOV-2002.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 18
ID   ABJ72279 standard; protein; 598 AA.
DE   Human PRO357 protein.
PN   US2003050448-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 19
ID   ABJ72407 standard; protein; 598 AA.
DE   Human PRO357 protein.
PN   US2003027988-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 20
ID   AB034302 standard; protein; 598 AA.
DE   Human secreted/transmembrane polypeptide PRO 357.
PN   US2003044934-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 21
ID   ABJ72109 standard; protein; 598 AA.
DE   Human membrane bound receptor/protein PRO357 amino acid sequence.
PN   US2003065147-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 22
ID   ADB83594 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003073814-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 23
ID   ADB80700 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003088068-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 24
ID   ADB73241 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003096968-A1.

PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 25
ID   ADB78323 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003092889-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 26
ID   ADB84971 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003073817-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 27
ID   ADB78077 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003092886-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 28
ID   ADB87143 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003088067-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 29
ID   ADB84725 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003092890-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 30
ID   ADB83840 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003069397-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 31
ID   ADB72995 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003092887-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 32
ID   ADC25825 standard; protein; 598 AA.
DE   Human secreted/transmembrane PRO polypeptide #12.
PN   US2002142419-A1.
PD   03-OCT-2002.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity   100.0%; Pred. No. 4.3e-190;

RESULT 33
ID   ADC25583 standard; protein; 598 AA.
DE   Human secreted/transmembrane PRO polypeptide #12.
PN   US2002156004-A1.
PD   24-OCT-2002.

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PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 34
ID   ADC25704 standard; protein; 598 AA.
DE   Human secreted/transmembrane PRO polypeptide #12.
PN   US2003077698-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 35
ID   ADC36833 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003080065-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 36
ID   ADC21823 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003096969-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 37
ID   ADC49854 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003088064-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 38
ID   ADC49053 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003088070-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 39
ID   ADC49570 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003088071-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 40
ID   ADC47431 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003088072-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 41
ID   ADC47176 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003105288-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 42
ID   ADC78051 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003096972-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.

     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 43
ID   ADD06286 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003073816-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 44
ID   ADC77805 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003088066-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 45
ID   ADD50768 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003105291-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 46
ID   ADD51014 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003105290-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 47
ID   ADD50495 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003096971-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 48
ID   ADD50249 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003096970-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 49
ID   ADD51260 standard; protein; 598 AA.
DE   Human secreted/transmembrane PRO polypeptide #12.
PN   US2003083479-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 50
ID   ADH27489 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003092888-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 7;  Length 598;
     Best Local Similarity   100.0%;  Pred. No. 4.3e-190;
RESULT 51
ID   ADC48807 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003099888-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 3135;  DB 8;  Length 598;
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Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 52
ID ADE20978 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 53
ID ADE05822 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 54
ID ADD75051 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 55
ID ADD75797 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 56
ID ADD85029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 57
ID ADD86855 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 58
ID ADE20732 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 59
ID ADE39029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 60
ID ADE05576 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;

RESULT 61
ID ADD73561 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 62
ID ADD78401 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 63
ID ADE21224 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 64
ID ADD77339 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 65
ID ADE20486 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 66
ID ADD75551 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 67
ID ADD74067 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 68
ID ADD74313 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 69
ID ADD76043 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 8; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 70

ID   ADD85535 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100721-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 71
ID   ADE05084 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003100726-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 72
ID   ADD75297 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003100714-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 73
ID   ADD76841 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100715-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 74
ID   ADD86609 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100719-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 75
ID   ADD78077 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100731-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 76
ID   ADB71538 standard; protein; 598 AA.
DE   Human secreted/transmembrane PRO polypeptide #12.
PN   US2003096742-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 77
ID   ADD77585 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100729-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 78
ID   ADD77831 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100730-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 79
ID   ADD85289 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100725-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 80
ID   ADD73821 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003100710-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 81
ID   ADD74559 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003100713-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 82
ID   ADD77087 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100716-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 83
ID   ADD85781 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100720-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 84
ID   ADE05330 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003100723-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 85
ID   ADD74805 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003100724-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 86
ID   ADG05617 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003096959-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 87
ID   ADG27171 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003096962-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 8; Length 598;
     Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 88
ID   ADG11234 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.

PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 89
ID ADG12013 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 90
ID ADF94570 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 91
ID ADG06666 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 92
ID ADG63481 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003211570-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 93
ID ADG39010 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 94
ID ADH43210 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003207401-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 95
ID ADG34100 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 96
ID ADI33570 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 97
ID ADH69664 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2004019183-A1.

PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 98
ID ADI29825 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 99
ID ADM27222 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 100
ID ADK65580 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 101
ID ADN00448 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2004091972-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 102
ID ADU25372 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2004220385-A1.
PD 04-NOV-2004.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 8; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 103
ID ADY39535 standard; protein; 598 AA.
DE Human insulin-like growth factor homolog PRO357 precursor protein.
PN US2005048613-A1.
PD 03-MAR-2005.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 9; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 104
ID ADY73816 standard; protein; 598 AA.
DE Human PRO357 protein, SEQ ID NO: 69.
PN WO2006026222-A2.
PD 09-MAR-2006.
PA (LEXI-) LEXICON GENETICS INC.
    Query Match   100.0%; Score 3135; DB 9; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 105
ID AEB19662 standard; protein; 598 AA.
DE Human secreted protein PRO357.
PN US2005059115-A1.
PD 17-MAR-2005.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 3135; DB 10; Length 598;
    Best Local Similarity   100.0%; Pred. No. 4.3e-190;
RESULT 106
ID AEH50165 standard; protein; 598 AA.
DE Human cDNA clone DNA44804-1248 protein product PRO357 SEQ ID NO: 69.
PN US2006105427-A1.

PD   18-MAY-2006.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 10; Length 598;
     Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 107
ID   AEH49290 standard; protein; 598 AA.
DE   Human secreted polypeptide PRO357, SEQ ID NO:104.
PN   EP1659177-A2.
PD   24-MAY-2006.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 10; Length 598;
     Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 108
ID   AEI36373 standard; protein; 598 AA.
DE   Human PRO protein amino acid sequence - SEQ ID 69.
PN   US2006127983-A1.
PD   15-JUN-2006.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 10; Length 598;
     Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 109
ID   AEK48325 standard; protein; 598 AA.
DE   Human PRO357 amino acid sequence.
PN   EP1686174-A1.
PD   02-AUG-2006.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 10; Length 598;
     Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 110
ID   AEK62918 standard; protein; 598 AA.
DE   Human PRO357 polypeptide, SEQ ID NO: 104.
PN   EP1700867-A2.
PD   13-SEP-2006.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 10; Length 598;
     Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 111
ID   AEL16958 standard; protein; 598 AA.
DE   Human secreted polypeptide PRO357, SEQ ID NO:104.
PN   EP1702928-A2.
PD   20-SEP-2006.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 3135; DB 10; Length 598;
     Best Local Similarity 100.0%; Pred. No. 4.3e-190;
RESULT 112
ID   AAY17831 standard; protein; 598 AA.
DE   Human PRO357 protein sequence.
PN   WO9928462-A2.
PD   10-JUN-1999.
PA   (GETH) GENENTECH INC.
     Query Match   99.7%; Score 3126; DB 2; Length 598;
     Best Local Similarity 99.8%; Pred. No. 1.6e-189;
RESULT 113
ID   AAB07428 standard; protein; 673 AA.
DE   Amino acid sequence of a leucine-rich surface glycoprotein (LRSG).
PN   WO200042170-A1.
PD   20-JUL-2000.
PA   (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
     Query Match   98.4%; Score 3083.5; DB 3; Length 673;
     Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 114
ID   AAB87533 standard; protein; 673 AA.
DE   Human PRO1282.
PN   WO200116318-A2.
PD   08-MAR-2001.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 4; Length 673;
     Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 115
ID   AAB65166 standard; protein; 673 AA.
DE   Human PRO1282 (UNQ652) protein sequence SEQ ID NO:52.
PN   WO200073454-A1.
PD   07-DEC-2000.

PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 4; Length 673;
     Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 116
ID   AAU75266 standard; protein; 673 AA.
DE   Human Slit-like protein #1.
PN   WO200212346-A2.
PD   14-FEB-2002.
PA   (PHAA) PHARMACIA CORP.
     Query Match   98.4%; Score 3083.5; DB 5; Length 673;
     Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 117
ID   ABG95858 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2002119130-A1.
PD   29-AUG-2002.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 5; Length 673;
     Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 118
ID   ABG78042 standard; protein; 673 AA.
DE   Human leucine-rich surface glycoprotein (LRSG-1).
PN   US2002072089-A1.
PD   13-JUN-2002.
PA   (HOLT/) HOLTZMAN D A.
PA   (MCCA/) MCCARTHY S A.
PA   (MACB/) MACBETH K J.
PA   (BUSF/) BUSFIELD S J.
PA   (PANY/) PAN Y.
PA   (WHIT/) WHITE D.
PA   (KHOD/) KHODADOUST M M.
PA   (GUWW/) GU W.
     Query Match   98.4%; Score 3083.5; DB 5; Length 673;
     Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 119
ID   ABU57981 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2003027163-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 120
ID   ABU59059 standard; protein; 673 AA.
DE   Novel human secreted or transmembrane protein PRO1282.
PN   US2002132252-A1.
PD   19-SEP-2002.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 121
ID   ABU82571 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003032023-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 122
ID   ABU60490 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein, #19.
PN   US2002160384-A1.
PD   31-OCT-2002.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 123
ID   ABU13872 standard; protein; 673 AA.
DE   Human PRO1282 polypeptide.
PN   US2002103125-A1.
PD   01-AUG-2002.
PA   (GETH) GENENTECH LTD.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 124

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ID   ABU72457 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003003531-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 125
ID   ABU90883 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003018173-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 126
ID   ABO33942 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003009013-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 127
ID   ABU71959 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003018183-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 128
ID   ABU71513 standard; protein; 673 AA.
DE   Human secreted polypeptide PRO1282.
PN   US2003013855-A1.
PD   16-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 129
ID   ABU72294 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2002182638-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 130
ID   ABU90967 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003018168-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 131
ID   ABU59206 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein, #19.
PN   US2003027162-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 132
ID   ABO25903 standard; protein; 673 AA.
DE   Human PRO1282 polypeptide.
PN   US2002127576-A1.
PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 133
ID   ABO27288 standard; protein; 673 AA.
DE   Human secreted/transmembrane polypeptide PRO1282.

PN   US2003009012-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 134
ID   ABU92483 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003045684-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 135
ID   ABU81153 standard; protein; 673 AA.
DE   Human secreted polypeptide PRO1282.
PN   US2003027212-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 136
ID   ABO53268 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003027986-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 137
ID   ABU58912 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein, #19.
PN   US2002142961-A1.
PD   03-OCT-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 138
ID   ABU92290 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003022187-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 139
ID   ABU59355 standard; protein; 673 AA.
DE   Novel human secreted or transmembrane protein PRO1282.
PN   US2003027985-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 140
ID   ABU98270 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2002183493-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 141
ID   ABU89275 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003036634-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 142
ID   ABU82482 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2002183494-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
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RESULT 143
ID   ABU92121 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003017476-A1.
PD   23-JAN-2003.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 144
ID   ABU96446 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003027993-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 145
ID   ABU10827 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2002123463-A1.
PD   05-SEP-2002.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 146
ID   ABU81579 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2002177164-A1.
PD   28-NOV-2002.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 147
ID   ABU72116 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003023042-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 148
ID   ABU88518 standard; protein; 673 AA.
DE   Human secreted and transmembrane polypeptide PRO1282.
PN   US2002197615-A1.
PD   26-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 149
ID   ABD17073 standard; protein; 673 AA.
DE   Human transmembrane PRO polypeptide (SeqID 16).
PN   US2003017981-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 150
ID   ABO34032 standard; protein; 673 AA.
DE   Human PRO1282 polypeptide.
PN   US2003008297-A1.
PD   09-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 151
ID   ADA37563 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003050462-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 152
ID   ADA21249 standard; protein; 673 AA.
DE   Human secreted/transmembrane polypeptide PRO1282.
PN   US2003054404-A1.
PD   20-MAR-2003.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 153
ID   ABO44246 standard; protein; 673 AA.
DE   Human secreted/transmembrane polypeptide PRO 1282.
PN   US2003018172-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 154
ID   ADA10036 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein, PRO1282.
PN   US2003059831-A1.
PD   27-MAR-2003.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 155
ID   ADA19878 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003069394-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 156
ID   ADB17261 standard; protein; 673 AA.
DE   Human transmembrane PRO polypeptide (SeqID 16).
PN   US2003050465-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 157
ID   ADA17580 standard; protein; 673 AA.
DE   Human PRO1282 polypeptide.
PN   US2003054987-A1.
PD   20-MAR-2003.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 158
ID   ADA27688 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003054359-A1.
PD   20-MAR-2003.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 159
ID   ADA20050 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003055222-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 160
ID   ABO34174 standard; protein; 673 AA.
DE   Human secreted/transmembrane polypeptide PRO 1282.
PN   US2003060601-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 9.1e-187;

RESULT 161
ID   ADA94268 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003059833-A1.
PD   27-MAR-2003.
Query Match   98.4%;   Score 3083.5;   DB 6;   Length 673;

Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 162
ID   ADA38493 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003059780-A1.
PD   27-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 163
ID   ADA92614 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003060407-A1.
PD   27-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 164
ID   ADA00347 standard; protein; 673 AA.
DE   Human secreted/transmembrane polypeptide PRO 1282.
PN   US2003027992-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 165
ID   ABO53118 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003044806-A1.
PD   06-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 166
ID   ADA22175 standard; protein; 673 AA.
DE   Human secreted/transmembrane polypeptide PRO1282.
PN   US2003040473-A1.
PD   27-FEB-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 167
ID   ABO22488 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003017982-A1.
PD   23-JAN-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 168
ID   ADA06341 standard; protein; 673 AA.
DE   Human secreted/transmembrane PRO polypeptide #13.
PN   US2003049638-A1.
PD   13-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 169
ID   ADA39034 standard; protein; 673 AA.
DE   Human secreted and transmembrane protein PRO1282.
PN   US2003059782-A1.
PD   27-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 170
ID   ADB85589 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003049735-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 171
ID   ADB96060 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2003054403-A1.
PD   20-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 172
ID   ADB68268 standard; protein; 673 AA.
DE   Human PRO1282 protein.
PN   US2003065161-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 173
ID   ADB68075 standard; protein; 673 AA.
DE   Human PRO1282 protein.
PN   US2003060600-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 174
ID   ADB90892 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003083473-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 175
ID   ADC57532 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2003027754-A1.
PD   06-FEB-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 176
ID   ADC54896 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2003045463-A1.
PD   06-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 177
ID   ADC11763 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003049681-A1.
PD   13-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 178
ID   ADC06972 standard; protein; 673 AA.
DE   Human PRO1282 protein.
PN   US2003060602-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 179
ID   ADC56185 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2003064375-A1.
PD   03-APR-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 180
ID   ADC17151 standard; protein; 673 AA.
DE   Mammalian PRO polypeptide (SeqID 16).
PN   US2003065143-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;
RESULT 181
ID   ADC07240 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003068647-A1.
PD   10-APR-2003.

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Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 182
ID   ADC11230 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003069403-A1.
PD   10-APR-2003.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 183
ID   ADC14849 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003073208-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 184
ID   ADC52344 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003138882-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 185
ID   ADC14352 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003082546-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 186
ID   ADD07884 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003066623-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 187
ID   ADC81709 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2003083461-A1.
PD   01-MAY-2003.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 188
ID   ADD07351 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2002193299-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 189
ID   ADC82242 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2003059833-A1.
PD   27-MAR-2003.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 190
ID   ADD08422 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003073090-A1.
PD   17-APR-2003.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 191
ID   ADD06671 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2002193300-A1.
PD   19-DEC-2002.

PA   (GETH ) GENENTECH INC.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 192
ID   ADC82918 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2003059783-A1.
PD   27-MAR-2003.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 193
ID   ADD55025 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2003077305-A1.
PD   24-APR-2003.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 194
ID   ADD36020 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003105298-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 195
ID   ADD55983 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2003077594-A1.
PD   24-APR-2003.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 196
ID   ADD54421 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2002132253-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 197
ID   ADE26575 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003087304-A1.
PD   08-MAY-2003.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 198
ID   ADE26042 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003087305-A1.
PD   08-MAY-2003.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 199
ID   ADF66979 standard; protein; 673 AA.
DE   Human PRO1282 amino acid sequence SEQ ID NO:52.
PN   US2002199148-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 200
ID   ADG01021 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003078387-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                98.4%;  Score 3083.5;  DB 7;  Length 673;
Best Local Similarity      88.7%;  Pred. No. 9.1e-187;
RESULT 201
ID   ADG08574 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
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PN   US2003180793-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 202
ID   ADF95195 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180795-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 203
ID   ADH24048 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180918-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 204
ID   ADH34074 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180858-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 205
ID   ADH29907 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180859-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 206
ID   ADH23878 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180919-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 207
ID   ADG85282 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180904-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 208
ID   ADH24558 standard; protein; 673 AA.
DE   Human secreted and transmembrane protein PRO1282.
PN   US2003181646-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 209
ID   ADH37414 standard; protein; 673 AA.
DE   Human secreted and transmembrane protein PRO1282.
PN   US2003180907-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 210
ID   ADH02003 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003180837-A1.

PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 211
ID   ADH37584 standard; protein; 673 AA.
DE   Human secreted and transmembrane protein PRO1282.
PN   US2003181648-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 212
ID   ADG85622 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180905-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 213
ID   ADH24218 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180914-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 214
ID   ADH38512 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181643-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 215
ID   ADG83633 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003180794-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 216
ID   ADH29441 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180860-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 217
ID   ADH27557 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180906-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 218
ID   ADH37754 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181647-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 7;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;

RESULT 219
ID   ADH37931 standard; protein; 673 AA.
DE   Human secreted and transmembrane protein PRO1282.
PN   US2003181649-A1.
PD   25-SEP-2003.
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PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 220
ID   ADH57351 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180920-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 221
ID   ADH53493 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181636-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 222
ID   ADH53663 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181641-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 223
ID   ADH51999 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181638-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 224
ID   ADH49854 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181639-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 225
ID   ADI25364 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181696-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 226
ID   ADH90157 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181698-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 227
ID   ADI25534 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181669-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 228
ID   ADH97708 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181672-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 229
ID   ADI35233 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2003050457-A1.
PD   13-MAR-2003.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 230
ID   ADI03556 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181656-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 231
ID   ADI11913 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181686-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 232
ID   ADH89987 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181697-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 233
ID   ADH99725 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003049682-A1.
PD   13-MAR-2003.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 234
ID   ADH98888 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181707-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 235
ID   ADI11063 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181682-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 236
ID   ADI11573 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181684-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 237
ID   ADH98218 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181709-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match            98.4%;    Score 3083.5;  DB 7;  Length 673;
Best Local Similarity  88.7%;    Pred. No. 9.1e-187;
RESULT 238
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ID   ADH98558 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181708-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 239
ID   ADH98048 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181673-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 240
ID   ADI05036 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180848-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 241
ID   ADI03386 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181654-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 242
ID   ADI04781 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181657-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 243
ID   ADH78235 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181668-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 244
ID   ADI19579 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181676-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 245
ID   ADH90327 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181699-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 246
ID   ADI03046 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181653-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 247
ID   ADH77895 standard; protein; 673 AA.

DE   Human PRO polypeptide #8.
PN   US2003181666-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 248
ID   ADH97878 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181674-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 249
ID   ADI01263 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003190669-A1.
PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 250
ID   ADI01958 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181652-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 251
ID   ADI03216 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181655-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 252
ID   ADI11403 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181681-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 253
ID   ADI02305 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181650-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 254
ID   ADI11743 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181685-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 255
ID   ADI05380 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003190716-A1.
PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity   88.7%; Pred. No. 9.1e-187;

RESULT 256
ID   ADH79452 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.

PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 257
ID ADI9409 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 258
ID ADI05210 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 259
ID ADH79622 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 260
ID ADI01448 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 261
ID ADI01618 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 262
ID ADI01788 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 263
ID ADH79792 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 264
ID ADI04610 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 265
ID ADI02746 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181651-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 266
ID ADH78065 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 267
ID ADI25704 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 268
ID ADI25874 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 269
ID ADK65386 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 270
ID ADH98728 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 271
ID ADH79969 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 272
ID ADL93700 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 273
ID ADC52154 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
        Query Match   98.4%; Score 3083.5; DB 7; Length 673;
        Best Local Similarity 88.7%; Pred. No. 9.1e-187;

RESULT 274
ID ADF35178 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.

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         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 275
ID   ADG11428 standard; protein; 673 AA.
DE   Human PRO1282 polypeptide.
PN   US2003228655-A1.
PD   11-DEC-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 276
ID   ADH06586 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180852-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 277
ID   ADH06416 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180853-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 278
ID   ADG68837 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180855-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 279
ID   ADH27727 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180912-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 280
ID   ADH25068 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180913-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 281
ID   ADH33700 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181645-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 282
ID   ADH02343 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003180839-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 283
ID   ADH07950 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180845-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;


         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 284
ID   ADG69347 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180846-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 285
ID   ADH39168 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180917-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 286
ID   ADG83908 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003180842-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 287
ID   ADH19298 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003228656-A1.
PD   11-DEC-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 288
ID   ADG85452 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003166848-A1.
PD   04-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 289
ID   ADH06246 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180854-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 290
ID   ADH30076 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180856-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 291
ID   ADH24388 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180910-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
RESULT 292
ID   ADG69517 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180844-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
         Query Match        98.4%;   Score 3083.5;   DB 8;   Length 673;
         Best Local Similarity  88.7%;   Pred. No. 9.1e-187;
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RESULT 293
ID   ADH07780 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180851-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 294
ID   ADG85792 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180861-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 295
ID   ADH39338 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180916-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 296
ID   ADH33530 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181637-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 297
ID   ADH33870 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181644-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 298
ID   ADH01080 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003180838-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 299
ID   ADG69687 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180843-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 300
ID   ADH20791 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein #8.
PN   US2003224358-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 301
ID   ADH02173 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003180841-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 302
ID   ADG69177 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180847-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 303
ID   ADG85962 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180862-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 304
ID   ADH24898 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180909-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 305
ID   ADH39515 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180915-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 306
ID   ADH19831 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003219856-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 307
ID   ADH02513 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003180840-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 308
ID   ADG69007 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180849-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 309
ID   ADH07610 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180850-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 310
ID   ADG86132 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180863-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;   Score 3083.5;   DB 8;   Length 673;
     Best Local Similarity   88.7%;   Pred. No. 9.1e-187;

RESULT 311
ID   ADH24728 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.

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PN   US2003180908-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 312
ID   ADH25776 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180911-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 313
ID   ADH38342 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180922-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 314
ID   ADH57181 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181642-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 315
ID   ADH52169 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180921-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 316
ID   ADH49535 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180857-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 317
ID   ADH90497 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181700-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 318
ID   ADI11233 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181683-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 319
ID   ADH98898 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003190698-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 320
ID   ADI02128 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003190699-A1.

PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 321
ID   ADH90667 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181701-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 322
ID   ADJ98542 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003187197-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 323
ID   ADJ98712 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003187228-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 324
ID   ADH78871 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181703-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 325
ID   ADJ99105 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003186408-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 326
ID   ADJ99275 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003187196-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 327
ID   ADH79041 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003187242-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 328
ID   ADJ98893 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181702-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity   88.7%;  Pred. No. 9.1e-187;
RESULT 329
ID   ADK00901 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003186407-A1.
PD   02-OCT-2003.
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PA (GETH) GENENTECH INC.
    Query Match   98.4%; Score 3083.5; DB 8; Length 673;
    Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 330
ID ADK14422 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US200318729-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   98.4%; Score 3083.5; DB 8; Length 673;
    Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 331
ID ADM80871 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
    Query Match   98.4%; Score 3083.5; DB 8; Length 673;
    Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 332
ID ADR45587 standard; protein; 673 AA.
DE Human leucine-rich surface glycoprotein, LRSG-1, protein #1.
PN US2004176296-A1.
PD 09-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
    Query Match   98.4%; Score 3083.5; DB 8; Length 673;
    Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 333
ID ADY77711 standard; protein; 673 AA.
DE Neoplastic disease detection protein PRO1282.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
    Query Match   98.4%; Score 3083.5; DB 9; Length 673;
    Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 334
ID AEA38367 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #81.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
    Query Match   98.4%; Score 3083.5; DB 9; Length 673;
    Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 335
ID AEF12542 standard; protein; 673 AA.
DE Human PRO1282 protein SEQ ID NO:16.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GETH) GENENTECH INC.
    Query Match   98.4%; Score 3083.5; DB 10; Length 673;
    Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 336
ID AEF74231 standard; protein; 673 AA.
DE Human PRO1282 protein SEQ ID NO:16.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W L.

    Query Match   98.4%; Score 3083.5; DB 10; Length 673;
    Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 337
ID AEH43569 standard; protein; 673 AA.
DE PRO1282 protein sequence, SEQ ID 16.
PN US200609657-A1.
PD 11-MAY-2006.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
    Query Match   98.4%; Score 3083.5; DB 10; Length 673;
    Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 338
ID AEJ11894 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2006160186-A1.
PD 20-JUL-2006.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
    Query Match   98.4%; Score 3083.5; DB 10; Length 673;
    Best Local Similarity 88.7%; Pred. No. 9.1e-187;
RESULT 339
ID AAB84689 standard; protein; 673 AA.
DE Amino acid sequence of human slit polypeptide Zslit3.
PN WO200146418-A1.
PD 28-JUN-2001.
PA (ZYMO) ZYMOGENETICS INC.
    Query Match   98.2%; Score 3078.5; DB 4; Length 673;
    Best Local Similarity 88.6%; Pred. No. 1.9e-186;
RESULT 340
ID ADF69108 standard; protein; 673 AA.
DE Human MP53 protein sequence SEQ ID NO:78.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
    Query Match   98.2%; Score 3078.5; DB 7; Length 673;
    Best Local Similarity 88.6%; Pred. No. 1.9e-186;
RESULT 341
ID AEL57287 standard; protein; 673 AA.
DE Human glomerulus-specific marker, SEQ ID NO: 1750.
PN US2006216722-A1.
PD 28-SEP-2006.
PA (BETS/) BETSHOLTZ C.
PA (TRYG/) TRYGGVASON K.
PA (TAKE/) TAKEMOTO M.
PA (HELL/) HE L.
PA (PATR/) PATRAKKAS J.
    Query Match   98.2%; Score 3078.5; DB 10; Length 673;
    Best Local Similarity 88.6%; Pred. No. 1.9e-186;
RESULT 342
ID ABO5949 standard; protein; 676 AA.
DE Human genome derived single exon protein #5683.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
    Query Match   98.2%; Score 3078.5; DB 8; Length 676;
    Best Local Similarity 88.6%; Pred. No. 1.9e-186;
RESULT 343

ID   ADA57213 standard; protein; 672 AA.
DE   Human secreted protein #496.
PN   WO200210294-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   93.6%; Score 2935; DB 6; Length 672;
     Best Local Similarity 85.2%; Pred. No. 2.3e-177;
RESULT 344
ID   ADA41092 standard; protein; 672 AA.
DE   Human secreted protein.
PN   WO200210293-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   93.6%; Score 2935; DB 6; Length 672;
     Best Local Similarity 85.2%; Pred. No. 2.3e-177;
RESULT 345
ID   ABR47923 standard; protein; 672 AA.
DE   Human secreted protein, SEQ ID 814.
PN   WO200295010-A2.
PD   28-NOV-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   93.6%; Score 2935; DB 6; Length 672;
     Best Local Similarity 85.2%; Pred. No. 2.3e-177;
RESULT 346
ID   AEL29423 standard; protein; 672 AA.
DE   Human secreted protein, SEQ ID 1403.
PN   US2006223088-A1.
PD   05-OCT-2006.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   93.6%; Score 2935; DB 10; Length 672;
     Best Local Similarity 85.2%; Pred. No. 2.3e-177;
RESULT 347
ID   AEL94636 standard; protein; 672 AA.
DE   Human secreted protein amino acid sequence - SEQ ID 817.
PN   US2006246483-A1.
PD   02-NOV-2006.
     Query Match   93.6%; Score 2935; DB 10; Length 672;
     Best Local Similarity 85.2%; Pred. No. 2.3e-177;
RESULT 348
ID   AAB38323 standard; protein; 673 AA.
DE   Human secreted protein encoded by gene 3 clone HSYAV50.
PN   WO200061623-A1.
PD   19-OCT-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   93.6%; Score 2935; DB 3; Length 673;
     Best Local Similarity 85.2%; Pred. No. 2.3e-177;
RESULT 349
ID   AAB38400 standard; peptide; 723 AA.
DE   Fragment of human secreted protein encoded by gene 3 clone HSYAV50.
PN   WO200061623-A1.
PD   19-OCT-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   93.6%; Score 2935; DB 3; Length 723;
     Best Local Similarity 85.2%; Pred. No. 2.5e-177;
RESULT 350
ID   AAU75267 standard; protein; 630 AA.
DE   Human slit-like protein #2.
PN   WO200212346-A2.
PD   14-FEB-2002.
PA   (PHAA) PHARMACIA CORP.
     Query Match   90.8%; Score 2845.5; DB 5; Length 630;
     Best Local Similarity 85.2%; Pred. No. 1e-171;
RESULT 351
ID   AAY66643 standard; protein; 611 AA.
DE   Membrane-bound protein PRO1282.
PN   WO9963088-A2.
PD   09-DEC-1999.
PA   (GETH) GENENTECH INC.
     Query Match   86.5%; Score 2712.5; DB 3; Length 611;
     Best Local Similarity 79.5%; Pred. No. 2.6e-163;
RESULT 352
ID   ABG78046 standard; protein; 673 AA.
DE   Mouse leucine-rich surface glycoprotein (LRSG-1).
PN   US2002072089-A1.

PD   13-JUN-2002.
PA   (HOLT/) HOLTZMAN D A.
PA   (MCCA/) MCCARTHY S A.
PA   (MACB/) MACBETH K J.
PA   (BUSF/) BUSFIELD S J.
PA   (PANY/) PAN Y.
PA   (WHIT/) WHITE D.
PA   (KHOD/) KHODADOUST M M.
PA   (GUVW/) GU W.
     Query Match   79.4%; Score 2490; DB 5; Length 673;
     Best Local Similarity 73.5%; Pred. No. 3.6e-149;
RESULT 353
ID   ADR45596 standard; protein; 673 AA.
DE   Human leucine-rich surface glycoprotein, LRSG-1, protein #2.
PN   US2004176296-A1.
PD   09-SEP-2004.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   79.4%; Score 2490; DB 8; Length 673;
     Best Local Similarity 73.5%; Pred. No. 3.6e-149;
RESULT 354
ID   AEL56067 standard; protein; 673 AA.
DE   Mouse slit-like 2, SEQ ID NO: 526.
PN   US2006216722-A1.
PD   28-SEP-2006.
PA   (BETS/) BETSHOLTZ C.
PA   (TRYG/) TRYGGVASON K.
PA   (TAKE/) TAKEMOTO M.
PA   (HELL/) HE L.
PA   (PATR/) PATRAKKAS J.
     Query Match   79.4%; Score 2490; DB 10; Length 673;
     Best Local Similarity 73.5%; Pred. No. 3.6e-149;
RESULT 355
ID   ADA00753 standard; protein; 673 AA.
DE   Murine stromal cell derived haematopoietin factor-5 SEQ ID NO:10.
PN   WO2003018805-A1.
PD   06-MAR-2003.
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA   (NINA-) JAPAN NAT CANCER CENT.
     Query Match   79.2%; Score 2484; DB 6; Length 673;
     Best Local Similarity 73.4%; Pred. No. 8.7e-149;
RESULT 356
ID   AAB07431 standard; protein; 493 AA.
DE   A leucine-rich surface glycoprotein (LRSG).
PN   WO200042170-A1.
PD   20-JUL-2000.
PA   (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
     Query Match   53.3%; Score 1672; DB 3; Length 493;
     Best Local Similarity 53.3%; Pred. No. 1.7e-97;
RESULT 357
ID   ABB72324 standard; protein; 281 AA.
DE   Rat protein isolated from skin cells SEQ ID NO: 648.
PN   WO200190357-A1.
PD   29-NOV-2001.
PA   (GENE-) GENESIS RES & DEV CORP LTD.
     Query Match   37.6%; Score 1178.5; DB 5; Length 281;
     Best Local Similarity 80.7%; Pred. No. 1.6e-66;
RESULT 358
ID   AAO30403 standard; protein; 311 AA.
DE   Human secreted protein (SECP)-6.
PN   WO2003046196-A1.
PD   05-JUN-2003.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   31.8%; Score 997.5; DB 7; Length 311;
     Best Local Similarity 68.7%; Pred. No. 5.3e-55;
RESULT 359
ID   ABR58506 standard; protein; 307 AA.
DE   Human secreted protein Incyte ID No: 7500228CD1 SEQ ID NO: 18.
PN   WO2003029437-A2.
PD   10-APR-2003.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   31.3%; Score 980.5; DB 6; Length 307;
     Best Local Similarity 67.9%; Pred. No. 6.2e-54;
RESULT 360

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ID   AAO30821 standard; protein; 117 AA.
DE   Human cell adhesion and extracellular matrix protein (CADECM)-11.
PN   WO2003047526-A2.
PD   12-JUN-2003.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             15.0%;  Score 471;  DB 7;  Length 117;
  Best Local Similarity   98.9%;  Pred. No. 3.8e-22;
RESULT 361
ID   AAB23980 standard; protein; 635 AA.
DE   Human LP220 secreted protein.
PN   WO200226801-A2.
PD   04-APR-2002.
PA   (ELIL ) LILLY & CO ELI.
  Query Match             11.5%;  Score 360.5;  DB 5;  Length 635;
  Best Local Similarity   27.1%;  Pred. No. 2.7e-14;
RESULT 362
ID   ABP70142 standard; protein; 647 AA.
DE   Human NOV44a.
PN   WO200272771-A2.
PD   19-SEP-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             11.5%;  Score 360.5;  DB 5;  Length 647;
  Best Local Similarity   27.1%;  Pred. No. 2.8e-14;
RESULT 363
ID   AAO26256 standard; protein; 635 AA.
DE   MDDT related human protein SEQ ID No 34.
PN   WO200296951-A1.
PD   05-DEC-2002.
PA   (INCY-) INCYTE GENOMICS INC.
  Query Match             11.5%;  Score 359.5;  DB 6;  Length 635;
  Best Local Similarity   27.6%;  Pred. No. 3.2e-14;
RESULT 364
ID   AD209859 standard; protein; 635 AA.
DE   Human breast cancer marker MGC3103 protein.
PN   EP1522594-A2.
PD   13-APR-2005.
PA   (FARB ) BAYER HEALTHCARE AG.
  Query Match             11.5%;  Score 359.5;  DB 6;  Length 635;
  Best Local Similarity   27.6%;  Pred. No. 3.2e-14;
RESULT 365
ID   ABP70144 standard; protein; 778 AA.
DE   Human NOV44c.
PN   WO200272771-A2.
PD   19-SEP-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             11.4%;  Score 357.5;  DB 5;  Length 778;
  Best Local Similarity   26.7%;  Pred. No. 5.4e-14;
RESULT 366
ID   ADM90979 standard; protein; 545 AA.
DE   Human pharmaceutically useful protein SeqID 372.
PN   WO200420595-A2.
PD   11-MAR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA   (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA   (DNAF-) DNAFORM KK.
  Query Match             11.2%;  Score 350.5;  DB 8;  Length 545;
  Best Local Similarity   27.9%;  Pred. No. 9.9e-14;
RESULT 367
ID   ABP70143 standard; protein; 566 AA.
DE   Human NOV44b.
PN   WO200272771-A2.
PD   19-SEP-2002.
PA   (CURA-) CURAGEN CORP.
  Query Match             10.8%;  Score 339;  DB 5;  Length 566;
  Best Local Similarity   26.9%;  Pred. No. 5.5e-13;
RESULT 368
ID   AAE17484 standard; protein; 551 AA.
DE   Human leucine-rich repeat-8 (ZLRR8) protein #2.
PN   WO200202604-A2.
PD   10-JAN-2002.
PA   (ZYMO ) ZYMOGENETICS INC.
  Query Match             10.8%;  Score 338;  DB 5;  Length 551;
  Best Local Similarity   27.4%;  Pred. No. 6.2e-13;

RESULT 369
ID   ADI21104 standard; protein; 618 AA.
DE   Novel human protein #79.
PN   WO2003025148-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
  Query Match             10.7%;  Score 337;  DB 7;  Length 618;
  Best Local Similarity   27.2%;  Pred. No. 8.2e-13;
RESULT 370
ID   ADA23287 standard; protein; 653 AA.
DE   Human SECX polypeptide, SECS #1.
PN   US2003054114-A1.
PD   20-MAR-2003.
PA   (SHIM/) SHIMKETS R A.
PA   (LARO/) LAROCHELLE W J.
  Query Match             10.7%;  Score 337;  DB 6;  Length 653;
  Best Local Similarity   23.6%;  Pred. No. 8.7e-13;
RESULT 371
ID   AAB23033 standard; protein; 694 AA.
DE   Human SLIT protein-like splice variant, SECX 3352358-1.
PN   WO200053742-A2.
PD   14-SEP-2000.
PA   (CURA-) CURAGEN CORP.
  Query Match             10.7%;  Score 337;  DB 3;  Length 694;
  Best Local Similarity   23.6%;  Pred. No. 9.4e-13;
RESULT 372
ID   AAB23034 standard; protein; 590 AA.
DE   Human SLIT protein-like splice variant, SECX 3352358-2.
PN   WO200053742-A2.
PD   14-SEP-2000.
PA   (CURA-) CURAGEN CORP.
  Query Match             10.6%;  Score 333;  DB 3;  Length 590;
  Best Local Similarity   25.8%;  Pred. No. 1.4e-12;
RESULT 373
ID   ADA23289 standard; protein; 590 AA.
DE   Human SECX polypeptide, SEC6.
PN   US2003054114-A1.
PD   20-MAR-2003.
PA   (SHIM/) SHIMKETS R A.
PA   (LARO/) LAROCHELLE W J.
  Query Match             10.6%;  Score 333;  DB 6;  Length 590;
  Best Local Similarity   25.8%;  Pred. No. 1.4e-12;
RESULT 374
ID   ABG04827 standard; protein; 526 AA.
DE   Novel human diagnostic protein #4818.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             10.6%;  Score 332;  DB 4;  Length 526;
  Best Local Similarity   26.9%;  Pred. No. 1.4e-12;
RESULT 375
ID   AAY28806 standard; protein; 653 AA.
DE   cc359_4 secreted protein.
PN   WO9950405-A1.
PD   07-OCT-1999.
PA   (GEMY ) GENETICS INST INC.
  Query Match             10.5%;  Score 330;  DB 2;  Length 653;
  Best Local Similarity   24.2%;  Pred. No. 2.4e-12;
RESULT 376
ID   AAY66694 standard; protein; 653 AA.
DE   Membrane-bound protein PRO1111.
PN   WO963088-A2.
PD   09-DEC-1999.
PA   (GETH ) GENENTECH INC.
  Query Match             10.5%;  Score 330;  DB 3;  Length 653;
  Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 377
ID   AAB24073 standard; protein; 653 AA.
DE   Human PRO1111 protein sequence SEQ ID NO:46.
PN   WO200053755-A2.
PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.
  Query Match             10.5%;  Score 330;  DB 3;  Length 653;
  Best Local Similarity   24.3%;
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          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 378
ID   AAU12390 standard; protein; 653 AA.
DE   Human PRO1111 polypeptide sequence.
PN   WO20014 0466-A2.
PD   07-JUN-2001.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 4;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 379
ID   AAE09438 standard; protein; 653 AA.
DE   Human sbgPRO331a protein.
PN   WO200160850-A1.
PD   23-AUG-2001.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
     Query Match    10.5%;    Score 330;    DB 4;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 380
ID   AAB65217 standard; protein; 653 AA.
DE   Human PRO1111 (UNQ554) protein sequence SEQ ID NO:229.
PN   WO200073454-A1.
PD   07-DEC-2000.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 4;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 381
ID   ABU58032 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003027163-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 382
ID   ABU59110 standard; protein; 653 AA.
DE   Novel human secreted or transmembrane protein PRO1111.
PN   US2002132252-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 383
ID   ABU82622 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003033023-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 384
ID   ABO17834 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003032156-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 385
ID   ABU60541 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein #93.
PN   US2002160384-A1.
PD   31-OCT-2002.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 386
ID   ABU13923 standard; protein; 653 AA.
DE   Human PRO1111 polypeptide.
PN   US2002103125-A1.
PD   01-AUG-2002.
PA   (GETH ) GENENTECH LTD.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 387


ID   ABU81088 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003004311-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 388
ID   ABU72508 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003003531-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 389
ID   ABU66788 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003036180-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 390
ID   AAO23105 standard; protein; 653 AA.
DE   NAG14 'human modifier of p53 pathway' protein.
PN   WO2003035833-A2.
PD   01-MAY-2003.
PA   (EXEL-) EXELIXIS INC.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 391
ID   ABU59869 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003017563-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 392
ID   ABU59257 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein, #93.
PN   US2003027162-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 393
ID   ABO25954 standard; protein; 653 AA.
DE   Human PRO1111 polypeptide.
PN   US2002127576-A1.
PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 394
ID   ABO25059 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein (PRO) #219.
PN   US2003036179-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 395
ID   ABU58963 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein, #93.
PN   US2002142961-A1.
PD   03-OCT-2002.
PA   (GETH ) GENENTECH INC.
     Query Match    10.5%;    Score 330;    DB 6;    Length 653
          Best Local Similarity  24.3%;    Pred. No. 2.4e-12;
RESULT 396
ID   ABU92341 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
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PN   US2003022187-A1.
PD   30-JAN-2003.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 397
ID   ABU59406 standard; protein; 653 AA.
DE   Novel human secreted or transmembrane protein PRO1344.
PN   US2003027985-A1.
PD   06-FEB-2003.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 398
ID   ABU67064 standard; protein; 653 AA.
DE   Human secreted/transmembrane, PRO, protein SEQ ID 438.
PN   US2003032155-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 399
ID   ABU92172 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003017476-A1.
PD   23-JAN-2003.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 400
ID   ABU10878 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2002123463-A1.
PD   05-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 401
ID   ABU81630 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2002177164-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 402
ID   ABU08569 standard; protein; 653 AA.
DE   Human secreted and transmembrane polypeptide PRO1111.
PN   US2002197615-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 403
ID   ABO34083 standard; protein; 653 AA.
DE   Human PRO1111 polypeptide.
PN   US2003017981-A1.
PD   23-JAN-2003.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 404
ID   ADA45957 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003022328-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 405
ID   ADA76388 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003073212-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;

RESULT 406
ID   ADA19038 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003054517-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 407
ID   ADA61661 standard; protein; 653 AA.
DE   Homo sapiens.
PN   US2003049816-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 408
ID   ADB19446 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003068796-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 409
ID   ADB27987 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082704-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 410
ID   ADA86466 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082711-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 411
ID   ADB16030 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003087350-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 412
ID   ADA37740 standard; protein; 653 AA.
DE   Human secreed/transmembrane protein PRO1111.
PN   US2003008297-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 413
ID   ADA47816 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003073215-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 414
ID   ADA21426 standard; protein; 653 AA.
DE   Human secreted/transmembrane polypeptide PRO1111.
PN   US2003054404-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;    Score 330; DB 6;  Length 653;
     Best Local Similarity 24.3%;   Pred. No. 2.4e-12;
RESULT 415
ID   ADA10213 standard; protein; 653 AA.
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DE   Human secreted/transmembrane protein, PRO1111.
PN   US2003059831-A1.
PD   27-MAR-2003.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 416
ID   ADA67611 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003068795-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 417
ID   ADB30618 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003068794-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 418
ID   ADA85914 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082693-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 419
ID   ADA17757 standard; protein; 653 AA.
DE   Human PRO1111 polypeptide.
PN   US2003054987-A1.
PD   20-MAR-2003.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 420
ID   ADA97126 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082705-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 421
ID   ADA79930 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082763-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 422
ID   ADA87569 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087345-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 423
ID   ADB16771 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003087349-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 424
ID   ADA27865 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003054359-A1.
PD   20-MAR-2003.

     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 425
ID   ADA91863 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082694-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 426
ID   ADB14926 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003087351-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 427
ID   ADB18887 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003073211-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 428
ID   ADA94102 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003077722-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 429
ID   ADB19998 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082691-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 430
ID   ADB13310 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082710-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 431
ID   ABO43367 standard; protein; 653 AA.
DE   Novel human secreted/transmembrane protein PRO1111.
PN   US2003044945-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 432
ID   ADA94445 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003059832-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 433
ID   ADA74564 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003068798-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 6; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;

RESULT 434
ID   ADB24797 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077713-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 435
ID   ADA82321 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082701-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 436
ID   ADA75284 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003073216-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 437
ID   ADA85362 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082695-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 438
ID   ADA84810 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082708-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 439
ID   ADB30066 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003073214-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 440
ID   ADA80594 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082761-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 441
ID   ADA75836 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082703-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 442
ID   ADA38670 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003059780-A1.
PD   27-MAR-2003.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 443
ID   ADA47061 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003073210-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 444
ID   ADB25357 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077715-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 445
ID   ADA93533 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003077721-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 446
ID   ADB26883 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003092147-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 447
ID   ADB31170 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003096386-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 448
ID   ADA92791 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003060407-A1.
PD   27-MAR-2003.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 449
ID   ADA61098 standard; protein; 653 AA.
DE   Homo sapiens.
PN   US2003049817-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 450
ID   ADB24245 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077714-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 451
ID   ADA96574 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082630-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;
     Best Local Similarity   24.3%;
     Score 330; DB 6; Length 653;
     Pred. No. 2.4e-12;

RESULT 452
ID   ADA81146 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082702-A1.

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PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 6;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 453
ID   ADA96022 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082759-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 6;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 454
ID   ADB26331 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082760-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 6;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 455
ID   ADB21816 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082765-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 6;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 456
ID   ADA77595 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003068797-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 457
ID   ADB18335 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003077710-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 458
ID   ADA87018 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082709-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 459
ID   ADA88121 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082700-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 460
ID   ADA46509 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003054516-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 461
ID   ADB28539 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082699-A1.
PD   01-MAY-2003.

PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 462
ID   ADB29091 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082706-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 463
ID   ABO53169 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003044806-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 464
ID   ADA77043 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003059909-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 465
ID   ADA22352 standard; protein; 653 AA.
DE   Human secreted/transmembrane polypeptide PRO1111.
PN   US2003040473-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 466
ID   ADA88673 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003073213-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 467
ID   ADA97678 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082686-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 468
ID   ADB27435 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003022239-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 469
ID   ADB22368 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087344-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 470
ID   ABO22539 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003017982-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 471
ID   ADA06518 standard; protein; 653 AA.
DE   Human secreted/transmembrane PRO polypeptide #64.
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PN   US2003049638-A1.
PD   13-MAR-2003.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 472
ID   ADA39211 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003059782-A1.
PD   27-MAR-2003.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 473
ID   ADA67059 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003068793-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 474
ID   ADB22920 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077711-A1.
PD   24-APR-2003.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 475
ID   ADB23693 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077712-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 476
ID   ADA92415 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082712-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 477
ID   ADB15478 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003087352-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 478
ID   ADB38730 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082766-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 479
ID   ADB96237 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003054403-A1.
PD   20-MAR-2003.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 480
ID   ADB38178 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087347-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;

     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 481
ID   ADB66650 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082689-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 482
ID   ADB89730 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082698-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 483
ID   ADB90462 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082762-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 484
ID   ADB39563 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082764-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 485
ID   ADB47186 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082687-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 486
ID   ADB86793 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082697-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 487
ID   ADB77398 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082696-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 488
ID   ADB34555 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077717-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 489
ID   ADB35659 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077719-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.4e-12;

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RESULT 490
ID   ADB34003 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077716-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 491
ID   ADB35107 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077718-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 492
ID   ADB36211 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077720-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 493
ID   ADB46606 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082692-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 494
ID   ADC57709 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003027754-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 495
ID   ADC55073 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003045463-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 496
ID   ADC11940 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003049681-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 497
ID   ADC07417 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003068647-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 498
ID   ADC56562 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003064375-A1.
PD   03-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 499
ID   ADC11407 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003069403-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;


RESULT 500
ID   ADC50479 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003092106-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 501
ID   ADC72026 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003092107-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 502
ID   ADC60005 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003092105-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 503
ID   ADC53012 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein Seq ID438.
PN   US2003087365-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 504
ID   ADC57366 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein Seq ID438.
PN   US2003087366-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 505
ID   ADC60557 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087367-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 506
ID   ADC51032 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087361-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 507
ID   ADC65559 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003087362-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          653 AA.
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 508
ID   ADC54657 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein Seq ID438.
PN   US2003087363-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
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RESULT 509
ID   ADC53618 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein Seq ID438.
PN   US2003087364-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 510
ID   ADC59141 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein Seq ID438.
PN   US2003087359-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 511
ID   ADC56019 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein Seq ID438.
PN   US2003087360-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 512
ID   ADC58589 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein Seq ID438.
PN   US2003087346-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 513
ID   ADC14529 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082546-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 514
ID   ADD08061 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003068623-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 515
ID   ADD03263 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003092104-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 516
ID   ADC90255 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087348-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 517
ID   ADC81886 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003083461-A1.
PD   01-MAY-2003.
RESULT 518
ID   ADC69674 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194770-A1.

PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 519
ID   ADC48563 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194773-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 520
ID   ADD10092 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194776-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 521
ID   ADD07528 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003193299-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 522
ID   ADD04667 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087354-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 523
ID   ADC82419 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003059833-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 524
ID   ADC80623 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003092103-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 525
ID   ADD11130 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194774-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 526
ID   ADC48011 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194771-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 527
ID   ADD08599 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003073090-A1.
PD   17-APR-2003.
     Query Match             10.5%;   Score 330; DB 7; Length 653;
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       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 528
ID   ADC80071 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087358-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 529
ID   ADD06848 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2002193300-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 530
ID   ADD09540 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194775-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 531
ID   ADC83095 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003059783-A1.
PD   27-MAR-2003.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 532
ID   ADD41253 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003203438-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 533
ID   ADD52392 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194769-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 534
ID   ADD53132 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194792-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 535
ID   ADD53684 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003203437-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 536
ID   ADD55202 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003077593-A1.
PD   24-APR-2003.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 537
ID   ADD56160 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003077594-A1.
PD   24-APR-2003.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 538
ID   ADD51840 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194779-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 539
ID   ADD02639 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003203431-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 540
ID   ADD02073 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003203430-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 541
ID   ADD54255 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003203432-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 542
ID   ADD54598 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2002132253-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 543
ID   ADD92572 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199030-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 544
ID   ADD91468 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199055-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 545
ID   ADE04082 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199057-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
       Query Match  10.5%;          Score 330;  DB 7;  Length 653;
       Best Local Similarity  24.3%;  Pred. No. 2.4e-12;   653 AA.
RESULT 546
ID   ADE26752 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087304-A1.
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PD   08-MAY-2003.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 547
ID   ADE32379 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003194765-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 548
ID   ADE22311 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199056-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 549
ID   ADD79535 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003203428-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 550
ID   ADE42071 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199023-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 551
ID   ADE17888 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199023-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 552
ID   ADD92020 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199053-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 553
ID   ADE33483 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003194767-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 554
ID   ADE34035 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003194791-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 555
ID   ADD80087 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207417-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 556
ID   ADD93124 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194768-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 557
ID   ADE19544 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199025-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 558
ID   ADE18992 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199026-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 559
ID   ADE43188 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199033-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 560
ID   ADD95977 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199059-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 561
ID   ADE22863 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199064-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 562
ID   ADD78981 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003203429-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 563
ID   ADE26219 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087305-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 564
ID   ADE32931 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003194766-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.4e-12;

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RESULT 565
ID   ADE42623 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199032-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 566
ID   ADD80639 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207418-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 567
ID   ADD89667 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199028-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 568
ID   ADE40951 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199031-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 569
ID   ADE04750 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199034-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 570
ID   ADE92879 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194477-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 571
ID   ADF67156 standard; protein; 653 AA.
DE   Human PRO1111 amino acid sequence SEQ ID NO:229.
PN   US2002198148-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 572
ID   ADG21588 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207355-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 573
ID   ADG23229 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207384-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 574

RESULT 575
ID   ADF97564 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207370-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 575
ID   ADG80628 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207373-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 576
ID   ADG80076 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207372-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 577
ID   ADH55368 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207381-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 578
ID   ADH55920 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207379-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 579
ID   ADI35410 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003050457-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 580
ID   ADI64139 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207385-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 581
ID   ADI65088 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207386-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 582
ID   ADI63587 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207387-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330; DB 7; Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.4e-12;
RESULT 583
ID   ADH82001 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
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PN  US2003207388-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 7; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 584
ID  ADH99902 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003049682-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 7; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 585
ID  ADH81449 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003207377-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 7; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 586
ID  ADM82618 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003087355-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 7; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 587
ID  ADN16017 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003087353-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 7; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 588
ID  ADN16646 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003087385-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 7; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 589
ID  ADN15465 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003087356-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 7; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 590
ID  ADN14913 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003087357-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 7; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 591
ID  ADC81175 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003092115-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 8; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 592
ID  ADD76623 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003100087-A1.
PD  29-MAY-2003.

PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 8; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 593
ID  ADD87987 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003092113-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 8; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 594
ID  ADD86191 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003203410-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 8; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 595
ID  ADE75839 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003211571-A1.
PD  13-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 8; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 596
ID  ADE23415 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003092108-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 8; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 597
ID  ADE23967 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003092110-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 8; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 598
ID  ADE24610 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003092111-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 8; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 599
ID  ADD87435 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003203439-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 8; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 600
ID  ADD89301 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003199062-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    10.5%;    Score 330; DB 8; Length 653;
    Best Local Similarity 24.3%; Pred. No. 2.4e-12;
RESULT 601
ID  ADE18440 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003194794-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
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     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 602
ID   ADE88749 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199054-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 603
ID   ADE94769 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199027-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 604
ID   ADE91180 standard; protein; 653 AA.
DE   Human PRO1111 polypeptide.
PN   US2003199061-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 605
ID   ADF35355 standard; protein; 653 AA.
DE   Human PRO1111 polypeptide.
PN   US2003194760-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 606
ID   ADE95321 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199052-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 607
ID   ADE93431 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199060-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 608
ID   ADF35012 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199029-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 609
ID   ADE92327 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003199051-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 610
ID   ADE90628 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199063-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;

RESULT 611
ID   ADE91775 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003199058-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 612
ID   ADG11605 standard; protein; 653 AA.
DE   Human PRO1111 polypeptide.
PN   US2003228655-A1.
PD   11-DEC-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 613
ID   ADG02354 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207352-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 614
ID   ADG22140 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207360-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 615
ID   ADG20210 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207376-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 616
ID   ADF98116 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207422-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 617
ID   ADG24333 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207426-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 618
ID   ADF98687 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003208055-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 619
ID   ADG03518 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207351-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 330;  DB 8;  Length 653;
     Best Local Similarity  24.3%;  Pred. No. 2.4e-12;
RESULT 620
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ID  ADF99239 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003207353-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 621
ID  ADG16824 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003207359-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 622
ID  ADG05283 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003207375-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 623
ID  ADG19550 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003207425-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 624
ID  ADG13387 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003207357-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 625
ID  ADG08444 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003207424-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 626
ID  ADG15614 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003219885-A1.
PD  27-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 627
ID  ADF97012 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003207371-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 628
ID  ADG06197 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003207374-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 629
ID  ADG23781 standard; protein; 653 AA.

DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003207389-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 630
ID  ADG04070 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003207423-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 631
ID  ADG24971 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003207427-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 632
ID  ADG07268 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003207350-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 633
ID  ADG07820 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003207356-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 634
ID  ADG55315 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003194778-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 635
ID  ADG60979 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003207390-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 636
ID  ADG62083 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
PN  US2003207428-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 637
ID  ADG82284 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2003207358-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match           10.5%;   Score 330; DB 8;  Length 653;
    Best Local Similarity  24.3%;   Pred. No. 2.4e-12;
RESULT 638
ID  ADG57523 standard; protein; 653 AA.
DE  Novel human secreted and transmembrane protein PRO1111.
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PN   US2003207362-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 639
ID   ADG56971 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207364-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 640
ID   ADG55867 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207365-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 641
ID   ADG58627 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207368-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 642
ID   ADG70993 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207420-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 643
ID   ADG58075 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207363-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 644
ID   ADG53659 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207421-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 645
ID   ADG71545 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207805-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 646
ID   ADG81732 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207805-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 647
ID   ADH19475 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003228656-A1.
PD   11-DEC-2003.

PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 648
ID   ADH30694 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003077723-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 649
ID   ADH12061 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207419-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 650
ID   ADG52483 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207414-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 651
ID   ADG54211 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207416-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 652
ID   ADG81180 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194793-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 653
ID   ADG56419 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207366-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 654
ID   ADG12685 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207378-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 655
ID   ADH20968 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003224358-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.4e-12;
RESULT 656
ID   ADG61531 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207429-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 330;   DB 8;   Length 653;

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       Best Local Similarity     24.3%;    Pred. No. 2.4e-12;
RESULT 657
ID   ADH20008 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003219856-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 658
ID   ADH28618 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003022331-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 659
ID   ADG54763 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207367-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 660
ID   ADG59803 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207369-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 661
ID   ADI81227 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207361-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 662
ID   ADG09970 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2004009548-A1.
PD   15-JAN-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 663
ID   ADI15441 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207382-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 664
ID   ADG09318 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2004009547-A1.
PD   15-JAN-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 665
ID   ADI14773 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207383-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;


RESULT 666
ID   ADI18368 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207349-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 667
ID   ADJ63649 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2004039164-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 668
ID   ADJ77544 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2004038336-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 669
ID   ADJ65666 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2004038135-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 670
ID   ADM27802 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2004048333-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 671
ID   ADM42526 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2004058424-A1.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 672
ID   ADM28388 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2004077064-A1.
PD   22-APR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 673
ID   ADI95870 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003077659-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 674
ID   ADI96422 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207354-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;    Score 330;  DB 8;  Length 653;
     Best Local Similarity   24.3%;    Pred. No. 2.4e-12;
RESULT 675
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ID   ADS32374 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2004203125-A1.
PD   14-OCT-2004.
PA   (GETH) GENENTECH INC.
Query Match   10.5%; Score 330; DB 8; Length 653;
Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 676
ID   ADT03358 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2004214269-A1.
PD   28-OCT-2004.
PA   (GETH) GENENTECH INC.
Query Match   10.5%; Score 330; DB 8; Length 653;
Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 677
ID   AD203409 standard; protein; 653 AA.
DE   Human secreted/transmembrane PRO1111 protein.
PN   US2005074837-A1.
PD   07-APR-2005.
PA   (GETH) GENENTECH INC.
Query Match   10.5%; Score 330; DB 9; Length 653;
Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 678
ID   AEA38492 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein, #132.
PN   US2005112725-A1.
PD   26-MAY-2005.
PA   (GETH) GENENTECH INC.
Query Match   10.5%; Score 330; DB 9; Length 653;
Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 679
ID   AEA23332 standard; protein; 653 AA.
DE   Tumor antigen of hematopoietic origin TAHO15.
PN   WO2005049075-A2.
PD   02-JUN-2005.
PA   (GETH) GENENTECH INC.
Query Match   10.5%; Score 330; DB 9; Length 653;
Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 680
ID   AEB14155 standard; protein; 653 AA.
DE   Cancer cell diagnosis method-related human protein - SEQ ID 438.
PN   US2005153396-A1.
PD   14-JUL-2005.
PA   (BAKE/) BAKER K P.
PA   (BERE/) BERESINI M.
PA   (DEFO/) DEFORGE L.
PA   (DESN/) DESNOYERS L.
PA   (FILV/) FILVAROFF E.
PA   (GAOW/) GAO W.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (SHER/) SHERWOOD S.
PA   (SMIT/) SMITH V.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W I.
PA   (ZHAN/) ZHANG Z.
Query Match   10.5%; Score 330; DB 9; Length 653;
Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 681
ID   AED86353 standard; protein; 653 AA.
DE   Human PRO amino acid sequence, seq id 438.
PN   US2005245730-A1.
PD   03-NOV-2005.
PA   (GETH) GENENTECH INC.
Query Match   10.5%; Score 330; DB 9; Length 653;
Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 682
ID   AEF79019 standard; protein; 653 AA.

DE   Human NAG14 polypeptide SEQ ID NO: 2.
PN   US2006035826-A1.
PD   16-FEB-2006.
PA   (LINJ/) LIN J C.
PA   (ROSE/) ROSENTHAL A.
Query Match   10.5%; Score 330; DB 10; Length 653;
Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 683
ID   AEG58300 standard; protein; 653 AA.
DE   Human PRO1111 polypeptide SEQ ID NO: 438.
PN   US2006073568-A1.
PD   06-APR-2006.
PA   (GETH) GENENTECH INC.
Query Match   10.5%; Score 330; DB 10; Length 653;
Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 684
ID   AEI43945 standard; protein; 653 AA.
DE   Human cancer-related PRO protein amino acid sequence - SEQ ID 438.
PN   US2006040351-A1.
PD   23-FEB-2006.
PA   (BAKE/) BAKER K P.
PA   (BERE/) BERESINI M.
PA   (DEFO/) DEFORGE L.
PA   (DESN/) DESNOYERS L.
PA   (FILV/) FILVAROFF E.
PA   (GAOW/) GAO W.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (SHER/) SHERWOOD S.
PA   (SMIT/) SMITH V.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W I.
PA   (ZHAN/) ZHANG Z.
Query Match   10.5%; Score 330; DB 10; Length 653;
Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 685
ID   AEI24028 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111, SEQ ID NO:438.
PN   EP1672070-A2.
PD   21-JUN-2006.
PA   (GETH) GENENTECH INC.
Query Match   10.5%; Score 330; DB 10; Length 653;
Best Local Similarity   24.3%; Pred. No. 2.4e-12;
RESULT 686
ID   ABU12069 standard; protein; 775 AA.
DE   Human NOV15a CG92531-01 protein SEQ ID 58.
PN   WO200281625-A2.
PD   17-OCT-2002.
PA   (CURA-) CURAGEN CORP.
Query Match   10.5%; Score 329.5; DB 6; Length 775;
Best Local Similarity   26.0%; Pred. No. 3.2e-12;
RESULT 687
ID   ABG98014 standard; protein; 649 AA.
DE   Human leucine rich repeat domain protein associated protein #1.
PN   WO200274959-A2.
PD   26-SEP-2002.
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match   10.5%; Score 329; DB 5; Length 649;
Best Local Similarity   24.6%; Pred. No. 2.8e-12;
RESULT 688
ID   ADS98753 standard; protein; 824 AA.
DE   Protein factor discovery related human contig polypeptide, SEQ ID 1017.
PN   WO2004087874-A2.
PD   14-OCT-2004.
PA   (NUVE-) NUVELO INC.
PA   (DRMA/) DRMANAC R T.
Query Match   10.5%; Score 329; DB 8; Length 824;
Best Local Similarity   25.5%; Pred. No. 3.7e-12;
RESULT 689

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ID   ABG34079 standard; protein; 627 AA.
DE   Human Pro peptide #51.
PN   WO20022488-A2.
PD   28-MAR-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 5;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 690
ID   ADA01368 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003068779-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 6;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 691
ID   ADA43797 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003064474-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 6;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 692
ID   ADA43565 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003073196-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 6;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 693
ID   ADA01240 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003068782-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 6;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 694
ID   ADA01124 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003068780-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 7;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 695
ID   ADA43681 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003073190-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 7;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 696
ID   ADA06943 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003068781-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 7;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 697
ID   ADA08431 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003068783-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 7;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 698
ID   ADB99724 standard; protein; 627 AA.

DE   Human PRO polypeptide SEQ ID 100.
PN   US2003082728-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 7;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 699
ID   ADB87007 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003082726-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 7;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 700
ID   ADB66162 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003082729-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 7;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 701
ID   ADB99840 standard; protein; 627 AA.
DE   Human PRO polypeptide SEQ ID 100.
PN   US2003073192-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 7;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 702
ID   ADB99495 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003082731-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 7;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 703
ID   ADB66046 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003082732-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 7;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 704
ID   ADC23444 standard; protein; 627 AA.
DE   Human transmembrane PRO polypeptide (SeqID 100).
PN   US2003073193-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 7;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 705
ID   ADC26137 standard; protein; 627 AA.
DE   Human PRO34192 protein.
PN   US2003073194-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 7;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 706
ID   ADE04964 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003068778-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;     Score 328.5;  DB 7;   Length 627;
     Best Local Similarity   24.2%;     Pred. No. 2.9e-12;
RESULT 707
ID   ADE11270 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
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PN   US2003073191-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 7;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 708
ID   ADD88201 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003082733-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 7;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 709
ID   ADD95496 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003064473-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 7;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 710
ID   ADE06426 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003073195-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 7;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 711
ID   ADE38201 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119120-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 7;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 712
ID   ADD88317 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003073189-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 7;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 713
ID   ADD90898 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003073188-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 7;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 714
ID   ADF99453 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003078401-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 7;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 715
ID   ADG06546 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003077742-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 7;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 716
ID   ADG05497 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003077741-A1.

PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 7;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 717
ID   ADG82498 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003077744-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 7;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 718
ID   ADE51751 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003104560-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 719
ID   ADE51867 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003104561-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 720
ID   ADE37725 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003104564-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 721
ID   ADE37609 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003104565-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 722
ID   ADD95380 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003138901-A1.
PD   24-JUL-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 723
ID   ADE38080 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003104566-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 724
ID   ADE76169 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003124665-A1.
PD   03-JUL-2003.
PA   (GETH) GENENTECH INC.
     Query Match 10.5%;   Score 328.5;   DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.9e-12;
RESULT 725
ID   ADE39492 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119117-A1.
PD   26-JUN-2003.

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PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;   Length 627
RESULT 726
ID   ADE04296 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003096364-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;   Length 627
RESULT 727
ID   ADE39893 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003138896-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;   Length 627
RESULT 728
ID   ADE19758 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003138903-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;   Length 627
RESULT 729
ID   ADE77336 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003124666-A1.
PD   03-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;   Length 627
RESULT 730
ID   ADE65444 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119916-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;   Length 627
RESULT 731
ID   ADE76053 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003124663-A1.
PD   03-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;   Length 627
RESULT 732
ID   ADE37964 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119119-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;   Length 627
RESULT 733
ID   ADE64574 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119114-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;   Length 627
RESULT 734
ID   ADE38909 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003096363-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.

     Query Match            10.5%;   Score 328.5;  DB 8;   Length 627
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;
RESULT 735
ID   ADE51983 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003104562-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;   Length 627
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;
RESULT 736
ID   ADD91014 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003138902-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;   Length 627
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;
RESULT 737
ID   ADE38793 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003108996-A1.
PD   12-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;   Length 627
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;
RESULT 738
ID   ADE37493 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003104563-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;   Length 627
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;
RESULT 739
ID   ADE06309 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003138898-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;   Length 627
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;
RESULT 740
ID   ADD90169 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003138904-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;   Length 627
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;
RESULT 741
ID   ADE38677 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119086-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;   Length 627
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;
RESULT 742
ID   ADE39608 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119118-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;   Length 627
     Best Local Similarity  24.2%;   Pred. No. 2.9e-12;
RESULT 743
ID   ADD89213 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003138897-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            10.5%;   Score 328.5;  DB 8;   Length 627
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Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 744
ID ADD88980 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 745
ID ADE19874 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 746
ID ADE77452 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 747
ID ADE65328 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 748
ID ADE39376 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 749
ID ADE38561 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 750
ID ADG11114 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 751
ID ADG10998 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 752
ID ADH31526 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;

RESULT 753
ID ADH38774 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 754
ID ADH29409 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 755
ID ADH23712 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 756
ID ADH27042 standard; protein; 627 AA.
DE Human secreted/transmembrane protein PRO34192.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 757
ID ADH38310 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 758
ID ADH26926 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 759
ID ADH38194 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 760
ID ADH38890 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 761
ID ADH23828 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.9e-12;
RESULT 762

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ID   ADH40203 standard; protein; 627 AA.
DE   Human PRO34192 protein.
PN   US2003119132-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 763
ID   ADH40088 standard; protein; 627 AA.
DE   Human PRO34192 protein.
PN   US2003119133-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 764
ID   ADH31410 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119138-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 765
ID   ADH29288 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003119136-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 766
ID   ADH49503 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119127-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 767
ID   ADH51967 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119125-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 768
ID   ADH49822 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119128-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 769
ID   ADH52423 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119130-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 770
ID   ADH52539 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119129-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 771
ID   ADH58536 standard; protein; 627 AA.

DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119121-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 772
ID   ADH51851 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119126-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 773
ID   ADH58412 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119122-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 774
ID   ADI13609 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119131-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 775
ID   ADK00865 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003186373-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 776
ID   ADL08606 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003186372-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 777
ID   AEG75266 standard; protein.
DE   Human PRO34192 protein.
PN   US2006073579-A1.
PD   06-APR-2006.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 10;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 778
ID   AEG74481 standard; protein; 627 AA.
DE   Human PRO34192 protein SEQ ID NO:100.
PN   US2006073553-A1.
PD   06-APR-2006.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 10;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 779
ID   AEG73353 standard; protein; 627 AA.
DE   Human PRO34192 protein.
PN   US2006073551-A1.
PD   06-APR-2006.
PA   (GETH ) GENENTECH INC.
     Query Match         10.5%;  Score 328.5;  DB 10;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.9e-12;
RESULT 780
ID   AEG74597 standard; protein; 627 AA.
DE   Human PRO34192 polypeptide SEQ ID NO:100.
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PN  US2006073552-A1.
PD  06-APR-2006.
PA  (GETH ) GENENTECH INC.
    Query Match     10.5%;  Score 328.5; DB 10;  Length 627;
    Best Local Similarity     24.2%;  Pred. No. 2.9e-12;
RESULT 781
ID  AAU32870 standard; protein; 636 AA.
DE  Novel human secreted protein #3361.
PN  WO200179449-A2.
PD  25-OCT-2001.
PA  (HYSE-) HYSEQ INC.
    Query Match     10.4%;  Score 327.5; DB 4;  Length 636;
    Best Local Similarity     24.2%;  Pred. No. 3.4e-12;
RESULT 782
ID  AB084499 standard; protein; 626 AA.
DE  Mouse cancer-associated protein MP14-035.1.
PN  WO2004074320-A2.
PD  02-SEP-2004.
PA  (SAGR-) SAGRES DISCOVERY INC.
    Query Match     10.3%;  Score 324; DB 8;  Length 626;
    Best Local Similarity     24.3%;  Pred. No. 5.5e-12;
RESULT 783
ID  AAG65805 standard; protein; 628 AA.
DE  Human leucine-rich repeat (LRR) family member, 33395 polypeptide.
PN  WO200172827-A2.
PD  04-OCT-2001.
PA  (MILL-) MILLENNIUM PHARM INC.
    Query Match     10.3%;  Score 324; DB 4;  Length 628;
    Best Local Similarity     24.1%;  Pred. No. 5.6e-12;
RESULT 784
ID  ADN95165 standard; protein; 810 AA.
DE  Human BEC/LEC-related protein sequence SeqID87.
PN  WO2003080640-A1.
PD  02-OCT-2003.
PA  (LUDW-) LUDWIG INST CANCER RES.
PA  (LICN ) LICENTIA LTD.
    Query Match     10.3%;  Score 322.5; DB 7;  Length 810;
    Best Local Similarity     24.1%;  Pred. No. 5.6e-12;
RESULT 785
ID  ABR58642 standard; protein; 811 AA.
DE  Human cancer related protein SEQ ID NO:299.
PN  WO2003025138-A2.
PD  27-MAR-2003.
PA  (EOSB-) EOS BIOTECHNOLOGY INC.
    Query Match     10.3%;  Score 322.5; DB 6;  Length 811;
    Best Local Similarity     22.0%;  Pred. No. 9.3e-12;
RESULT 786
ID  AAO23114 standard; protein; 811 AA.
DE  KIAA0644 'human modifier of p53 pathway' protein.
PN  WO2003035833-A2.
PD  01-MAY-2003.
PA  (EXEL-) EXELIXIS INC.
    Query Match     10.3%;  Score 322.5; DB 6;  Length 811;
    Best Local Similarity     22.0%;  Pred. No. 9.3e-12;
RESULT 787
ID  ADN95110 standard; protein; 811 AA.
DE  Human LEC protein sequence SeqID32.
PN  WO2003080640-A1.
PD  02-OCT-2003.
PA  (LUDW-) LUDWIG INST CANCER RES.
PA  (LICN ) LICENTIA LTD.
    Query Match     10.3%;  Score 322.5; DB 7;  Length 811;
    Best Local Similarity     22.0%;  Pred. No. 9.3e-12;
RESULT 788
ID  ADQ21196 standard; protein; 811 AA.
DE  Human soft tissue sarcoma-upregulated protein - SEQ ID 4016.
PN  WO2004048938-A2.
PD  10-JUN-2004.
PA  (PROT-) PROTEIN DESIGN LABS INC.
    Query Match     10.3%;  Score 322.5; DB 8;  Length 811;
    Best Local Similarity     22.0%;  Pred. No. 9.3e-12;
RESULT 789
ID  AEL77006 standard; protein; 811 AA.


DE  Toll-like receptor/Interleukin-1 receptor 14 (TLR14) SEQ ID NO 1.
PN  WO200611946-A2.
PD  26-OCT-2006.
PA  (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
    Query Match     10.3%;  Score 322.5;  DB 10;  Length 811;
    Best Local Similarity     22.0%;  Pred. No. 9.3e-12;
RESULT 790
ID  ADR45590 standard; protein; 605 AA.
DE  Homologue of LRSG-1, baboon ALS.
PN  US200417296-A1.
PD  09-SEP-2004.
PA  (MILL-) MILLENNIUM PHARM INC.
    Query Match     10.3%;  Score 322; DB 8;  Length 605;
    Best Local Similarity     36.2%;  Pred. No. 7.1e-12;
RESULT 791
ID  AAG67523 standard; protein; 628 AA.
DE  Amino acid sequence of a human secreted polypeptide.
PN  WO200166690-A2.
PD  13-SEP-2001.
PA  (SMIK ) SMITHKLINE BEECHAM CORP.
PA  (SMIK ) SMITHKLINE BEECHAM PLC.
    Query Match     10.2%;  Score 321; DB 4;  Length 628;
    Best Local Similarity     23.9%;  Pred. No. 8.6e-12;
RESULT 792
ID  AAB84469 standard; protein; 628 AA.
DE  Amino acid sequence of an interferon omega-1 like protein NOV2.
PN  WO200142471-A2.
PD  14-JUN-2001.
PA  (CURA-) CURAGEN CORP.
    Query Match     10.2%;  Score 321; DB 4;  Length 628;
    Best Local Similarity     23.9%;  Pred. No. 8.6e-12;
RESULT 793
ID  ABP69326 standard; protein; 628 AA.
DE  Human polypeptide SEQ ID NO 1373.
PN  WO200270539-A2.
PD  12-SEP-2002.
PA  (HYSE-) HYSEQ INC.
    Query Match     10.2%;  Score 321; DB 5;  Length 628;
    Best Local Similarity     23.9%;  Pred. No. 8.6e-12;
RESULT 794
ID  ADF69107 standard; protein; 628 AA.
DE  Human MP53 protein sequence SEQ ID NO:77.
PN  WO2003083047-A2.
PD  09-OCT-2003.
PA  (EXEL-) EXELIXIS INC.
    Query Match     10.2%;  Score 321; DB 7;  Length 628;
    Best Local Similarity     23.9%;  Pred. No. 8.6e-12;
RESULT 795
ID  ADH71652 standard; protein; 628 AA.
DE  Human protein of the invention NOV22a SEQ ID NO:548.
PN  WO2003102155-A2.
PD  11-DEC-2003.
PA  (CURA-) CURAGEN CORP.
    Query Match     10.2%;  Score 321; DB 8;  Length 628;
    Best Local Similarity     23.9%;  Pred. No. 8.6e-12;
RESULT 796
ID  ADH71654 standard; protein; 628 AA.
DE  Human protein of the invention NOV22b SEQ ID NO:550.
PN  WO2003102155-A2.
PD  11-DEC-2003.
PA  (CURA-) CURAGEN CORP.
    Query Match     10.2%;  Score 321; DB 8;  Length 628;
    Best Local Similarity     23.9%;  Pred. No. 8.6e-12;
RESULT 797
ID  AB084502 standard; protein; 628 AA.
DE  Human cancer-associated protein HP14-035.3.
PN  WO2004074320-A2.
PD  02-SEP-2004.
PA  (SAGR-) SAGRES DISCOVERY INC.
    Query Match     10.2%;  Score 321; DB 8;  Length 628;
    Best Local Similarity     23.9%;  Pred. No. 8.6e-12;
RESULT 798
ID  AB084503 standard; protein; 628 AA.
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DE Human cancer-associated protein HP14-035.4.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
    Query Match   10.2%;   Score 321;   DB 8;   Length 628;
    Best Local Similarity   23.9%;   Pred. No. 8.6e-12;
RESULT 799
ID ABO84501 standard; protein; 628 AA.
DE Human cancer-associated protein HP14-035.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
    Query Match   10.2%;   Score 321;   DB 8;   Length 628;
    Best Local Similarity   23.9%;   Pred. No. 8.6e-12;
RESULT 800
ID ABP70928 standard; protein.
DE Human LP341 protein.
PN WO2003029778-A2.
PD 10-APR-2003.
PA (ELIL) LILLY & CO ELI.
    Query Match   10.2%;   Score 321;   DB 6;   Length 762;
    Best Local Similarity   25.5%;   Pred. No. 1.1e-11;
RESULT 801
ID ADI36917 standard; protein; 797 AA.
DE Human LRR protein #12.
PN US2003220263-A1.
PD 27-NOV-2003.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
    Query Match   10.2%;   Score 321;   DB 8;   Length 797;
    Best Local Similarity   25.5%;   Pred. No. 1.1e-11;
RESULT 802
ID ADS98018 standard; protein; 803 AA.
DE Protein factor discovery related isolated human polypeptide, SEQ ID 282.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
    Query Match   10.2%;   Score 321;   DB 8;   Length 803;
    Best Local Similarity   25.5%;   Pred. No. 1.1e-11;
RESULT 803
ID AAY13349 standard; protein; 660 AA.
DE Amino acid sequence of protein PRO265.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320;   DB 2;   Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 804
ID ADC78348 standard; protein; 660 AA.
DE Human PRO265 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320;   DB 3;   Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 805
ID AAB80217 standard; protein; 660 AA.
DE Human PRO265 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320;   DB 4;   Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 806
ID AAB31208 standard; protein; 660 AA.
DE Amino acid sequence of human polypeptide PRO265.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320;   DB 4;   Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;

RESULT 807
ID AAU12346 standard; protein; 660 AA.
DE Human PRO265 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320;   DB 4;   Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 808
ID ABB84839 standard; protein; 660 AA.
DE Human PRO265 protein sequence SEQ ID NO:46.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320;   DB 5;   Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 809
ID ABB95445 standard; protein; 660 AA.
DE Human angiogenesis related protein PRO265 SEQ ID NO: 46.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
    Query Match   10.2%;   Score 320;   DB 5;   Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 810
ID ABU71595 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320;   DB 6;   Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 811
ID ABO17790 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320;   DB 6;   Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 812
ID ABU71450 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320;   DB 6;   Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 813
ID ABO25179 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320;   DB 6;   Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 814
ID ABU81044 standard; protein; 660 AA.

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DE   Human PRO polypeptide #175.
PN   US2003004311-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 815
ID   ABU71896 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein PRO265.
PN   US2003005530-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 816
ID   ABO01779 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2002197165-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 817
ID   ABU66744 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003036180-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 818
ID   ABU54352 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein PRO265.
PN   US2002132240-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 819
ID   ABU67297 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003032063-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 820
ID   AAO23116 standard; protein; 660 AA.
DE   FLRT2 'human modifier of p53 pathway' protein.
PN   WO2003035833-A2.
PD   01-MAY-2003.
PA   (EXEL-) EXELIXIS INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 821
ID   ABO47367 standard; protein; 660 AA.
DE   Human secreted/transmembrane polypeptide PRO265.
PN   US2003044839-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 822
ID   ABU59825 standard; protein; 660 AA.
DE   Novel secreted and transmembrane protein PRO265.
PN   US2003017563-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 823
ID   ABO25015 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein (PRO) #175.

PN   US2003036179-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 824
ID   ABU64504 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2002160374-A1.
PD   31-OCT-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 825
ID   ABU72065 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2002177165-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 826
ID   ABU67350 standard; protein; 660 AA.
DE   Human secreted protein PRO265.
PN   US2003023054-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 827
ID   ABU67166 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003032062-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 828
ID   ABO14870 standard; protein; 660 AA.
DE   Human secreted / transmembrane polypeptide PRO265.
PN   US2003036060-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 829
ID   ABU67020 standard; protein; 660 AA.
DE   Human secreted/transmembrane, PRO, protein SEQ ID 350.
PN   US2003032155-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 830
ID   ABU69627 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003017463-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 831
ID   ABU79808 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein PRO265.
PN   US2003032057-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 1.1e-11;
RESULT 832
ID   ABO14809 standard; protein; 660 AA.
DE   Human secreted / transmembrane polypeptide PRO265.
PN   US2003027143-A1.
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PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 833
ID   ADA45869 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003022328-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 834
ID   ADA76300 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003073212-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 835
ID   ADB29233 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003092002-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 836
ID   ADA18950 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003054517-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 837
ID   ADA61573 standard; protein; 660 AA.
DE   Homo sapiens.
PN   US2003049816-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 838
ID   ADB19358 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003068796-A1..
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 839
ID   ADB27899 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082704-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 840
ID   ADA86378 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082711-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 841
ID   ADB15942 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003087350-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 842
ID   ADA47728 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003073215-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 843
ID   ADA18089 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003039971-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 844
ID   ABO32761 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein PRO265.
PN   US2003045693-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 845
ID   ADA67523 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003068795-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 846
ID   ADB30530 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003068794-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 847
ID   ADA85826 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082693-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 848
ID   ADA97038 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082705-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 849
ID   ADA79342 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082763-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match     10.2%;   Score 320;   DB 6;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 850
ID   ADA87481 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003087345-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
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Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 851
ID   ADB16683 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003087349-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 852
ID   ABO34821 standard; protein; 660 AA.
DE   Human PRO polypeptide #6.
PN   US2003044793-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 853
ID   ADA16064 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003049621-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 854
ID   ADA91775 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082694-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 855
ID   ADB14838 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003087351-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 856
ID   ADA47287 standard; protein; 660 AA.
DE   Novel human secreted/transmembrane polypeptide PRO265.
PN   US2003044884-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 857
ID   ADB18799 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003073211-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 858
ID   ADA94014 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003077722-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 859
ID   ADB19910 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082691-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;

Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 860
ID   ADB13222 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082710-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 861
ID   ABO43323 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003044945-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 862
ID   ADA74476 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003068798-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 863
ID   ADA42209 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003054401-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 864
ID   ADB24709 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077713-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 865
ID   ADA82233 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082701-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 866
ID   ADA75196 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003072695-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 867
ID   ADA85274 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003073216-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
RESULT 868
ID   ADA84722 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082708-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity  22.4%;  Pred. No. 1.1e-11;
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RESULT 869
ID   AB017499 standard; protein; 660 AA.
DE   Human PRO polypeptide #6.
PN   US2003064367-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 870
ID   ADB29978 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003073214-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 871
ID   ADA80506 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082761-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 872
ID   ADA75748 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082703-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 873
ID   ADA46973 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003073210-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 874
ID   ADB25269 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077715-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 875
ID   ADA93445 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003077721-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 876
ID   ADB26795 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003092147-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 877
ID   ADB31082 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003096386-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 878
ID   ADA61010 standard; protein; 660 AA.
DE   Homo sapiens.
PN   US2003049817-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 879
ID   ADB24157 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077714-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 880
ID   ADA96486 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082690-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 881
ID   ADA81058 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082702-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 882
ID   ADA95934 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082759-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 883
ID   ADB26243 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082760-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 884
ID   ADB21728 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082765-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 6;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 885
ID   ADA77507 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003068797-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 7;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 886
ID   ADB18247 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003077710-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;          Score 320;  DB 7;  Length 660;
     Best Local Similarity 22.4%;      Pred. No. 1.1e-11;
RESULT 887
ID   ADA86930 standard; protein; 660 AA.
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DE    Novel human secreted and transmembrane protein PRO265.
PN    US2003082709-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 888
ID    ADA16488 standard; protein; 660 AA.
DE    Human secreted/transmembrane protein, #7.
PN    US2003039969-A1.
PD    27-FEB-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 889
ID    ADA12917 standard; protein; 660 AA.
DE    Human secreted/transmembrane protein, #7.
PN    US2003049622-A1.
PD    13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 890
ID    ADA41785 standard; protein; 660 AA.
DE    Human secreted/transmembrane protein, #7.
PN    US2003082540-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 891
ID    ADA88033 standard; protein; 660 AA.
DE    Novel human secreted and transmembrane protein PRO265.
PN    US2003082700-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 892
ID    ADA46421 standard; protein; 660 AA.
DE    Novel human secreted and transmembrane protein PRO265.
PN    US2003054516-A1.
PD    20-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 893
ID    ADA17132 standard; protein; 660 AA.
DE    Human secreted/transmembrane protein, #7.
PN    US2003017498-A1.
PD    23-JAN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 894
ID    ADA42635 standard; protein; 660 AA.
DE    Human secreted/transmembrane protein, #7.
PN    US2003054351-A1.
PD    20-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 895
ID    ADB28451 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003082699-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 896
ID    ADB29003 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.

PN    US2003082706-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 897
ID    ADA76955 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003059909-A1.
PD    27-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 898
ID    ADA88585 standard; protein; 660 AA.
DE    Novel human secreted and transmembrane protein PRO265.
PN    US2003073213-A1.
PD    17-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 899
ID    ADA97590 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003082686-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 900
ID    ADB27347 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003022239-A1.
PD    30-JAN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 901
ID    ADB22280 standard; protein; 660 AA.
DE    Novel human secreted and transmembrane protein PRO265.
PN    US2003087344-A1.
PD    08-MAY-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 902
ID    ABO19866 standard; protein; 660 AA.
DE    Human secreted/transmembrane protein PRO265.
PN    US2003049902-A1.
PD    06-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 903
ID    ABO17560 standard; protein; 660 AA.
DE    Human PRO polypeptide #6.
PN    US2003064923-A1.
PD    03-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 904
ID    ADA66971 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003068793-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match            10.2%;    Score 320;    DB 7;    Length 660;
      Best Local Similarity  22.4%;    Pred. No. 1.1e-11;
RESULT 905
ID    ADB22832 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003077711-A1.
PD    24-APR-2003.
PA    (GETH ) GENENTECH INC.
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Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 906
ID   ADB23605 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077712-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 907
ID   ADA92327 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082712-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 908
ID   ADB15390 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003087352-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 909
ID   ADB38642 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082766-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 910
ID   ADB38090 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003087347-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 911
ID   ADB66562 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082689-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 912
ID   ADB89642 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082762-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 913
ID   ADB90374 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003077654-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
RESULT 914
ID   ADB77554 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003077654-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 915
ID   ADB39475 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082764-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 916
ID   ADB74690 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003082542-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 917
ID   ADB47098 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082687-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 918
ID   ADB86705 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082697-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 919
ID   ADB77310 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082696-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 920
ID   ADB34467 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077717-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 921
ID   ADB35571 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077719-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 922
ID   ADB33915 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077716-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
RESULT 923
ID   ADB35019 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077718-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          10.2%;  Score 320; DB 7; Length 660;
Best Local Similarity 22.4%;  Pred. No. 1.1e-11;
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RESULT 924
ID ADB36123 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 925
ID ADB46518 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 926
ID ADC28336 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 927
ID ADC39536 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 928
ID ADC40050 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 929
ID ADC18878 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 930
ID ADC34174 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 931
ID ADC29229 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 932
ID ADC28760 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 933

ID ADC40645 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 934
ID ADC19302 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 935
ID ADC33750 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 936
ID ADC12820 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 937
ID ADC50391 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 938
ID ADC71938 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 939
ID ADC59917 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 940
ID ADC52924 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 941
ID ADC57278 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 942
ID ADC60469 standard; protein; 660 AA.

DE Novel human secreted and transmembrane protein PRO265.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 943
ID ADC50944 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 944
ID ADC65471 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 945
ID ADC54569 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 946
ID ADC53530 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 947
ID ADC59053 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 948
ID ADC55931 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 949
ID ADC58501 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 950
ID ADC12272 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 951
ID ADD0175 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.

PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 952
ID ADC90167 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 953
ID ADC69586 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 954
ID ADC48475 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 955
ID ADD10004 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 956
ID ADD04579 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 957
ID ADC80535 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 958
ID ADD11042 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 959
ID ADD10335 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%; Score 320; DB 7; Length 660;
    Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 960
ID ADC47923 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194771-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 961
ID ADD04827 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 962
ID ADC79983 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 963
ID ADD11295 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 964
ID ADD09452 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 965
ID ADD03833 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 966
ID ADD03409 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 967
ID ADD41165 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 968
ID ADD52304 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 969
ID ADD53044 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194792-A1.
PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 970
ID ADD53596 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 971
ID ADD37088 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 972
ID ADD51752 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 973
ID ADD02551 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 974
ID ADD01985 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 975
ID ADD54167 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 976
ID ADD92484 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 977
ID ADD91380 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.2%;   Score 320; DB 7; Length 660;
    Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 978
ID ADE03994 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

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      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 979
ID    ADE32291 standard; protein; 660 AA.
DE    Novel human secreted and transmembrane protein PRO265.
PN    US2003194765-A1.
PD    16-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 980
ID    ADE22223 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003199056-A1.
PD    23-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 981
ID    ADD79447 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003203428-A1.
PD    30-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 982
ID    ADE41983 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003194772-A1.
PD    16-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 983
ID    ADE17800 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003199023-A1.
PD    23-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 984
ID    ADD91932 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003199053-A1.
PD    23-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 985
ID    ADE33395 standard; protein; 660 AA.
DE    Novel human secreted and transmembrane protein PRO265.
PN    US2003194767-A1.
PD    16-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 986
ID    ADE33947 standard; protein; 660 AA.
DE    Novel human secreted and transmembrane protein PRO265.
PN    US2003194791-A1.
PD    16-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 987
ID    ADD79999 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003207417-A1.
PD    06-NOV-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;

      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 988
ID    ADD93036 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003194768-A1.
PD    16-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 989
ID    ADE19456 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003199025-A1.
PD    23-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 990
ID    ADE34661 standard; protein; 660 AA.
DE    Human secreted/transmembrane protein, #7.
PN    US2003077583-A1.
PD    24-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 991
ID    ADE18904 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003199026-A1.
PD    23-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 992
ID    ADE41100 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003199033-A1.
PD    23-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 993
ID    ADD95889 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003199059-A1.
PD    23-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 994
ID    ADE22775 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003199064-A1.
PD    23-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 995
ID    ADD78893 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003203429-A1.
PD    30-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
RESULT 996
ID    ADE32843 standard; protein; 660 AA.
DE    Novel human secreted and transmembrane protein PRO265.
PN    US2003194766-A1.
PD    16-OCT-2003.
PA    (GETH ) GENENTECH INC.
      Query Match                    10.2%;  Score 320; DB 7; Length 660;
      Best Local Similarity          22.4%;  Pred. No. 1.1e-11;
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RESULT 997
ID   ADE42535 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199032-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 998
ID   ADD80551 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207418-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 999
ID   ADD89579 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199028-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1000
ID   ADE40863 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199031-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1001
ID   ADE04662 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199034-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1002
ID   ADE92791 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003194777-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1003
ID   ADG21500 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207355-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1004
ID   ADG23141 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207384-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1005
ID   ADF97476 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207370-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1006
ID   ADG80540 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207373-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1007
ID   ADG79988 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207372-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1008
ID   ADG63796 standard; protein; 660 AA.
DE   Human secreted/transmembrane polypeptide PRO265.
PN   US2003170721-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1009
ID   ADH59144 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003039972-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1010
ID   ADH55280 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207381-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1011
ID   ADH55832 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207379-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1012
ID   ADI37923 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003054352-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1013
ID   ADI65000 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207386-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1014
ID   ADI63499 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207387-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;
     Best Local Similarity   22.4%;
     Score 320; DB 7; Length 660;
     Pred. No. 1.1e-11;
RESULT 1015
ID   ADH81913 standard; protein; 660 AA.
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DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207388-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 7;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1016
ID   ADH81361 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207377-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 7;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1017
ID   ADJ26191 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003054349-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 7;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1018
ID   ADM2530 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003087355-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 7;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1019
ID   ADN15929 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003087353-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 7;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1020
ID   ADN16558 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003087385-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 7;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1021
ID   ADN15377 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003087356-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 7;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1022
ID   ADN14825 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003087357-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 7;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1023
ID   ADI64051 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207385-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 7;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1024
ID   ADC81087 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.

PN   US2003092115-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1025
ID   ADE79106 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003135025-A1.
PD   17-JUL-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1026
ID   ADD76535 standard; protein #175.
DE   Human PRO polypeptide #175.
PN   US2003100087-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1027
ID   ADD87899 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003092113-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1028
ID   ADD86303 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003203440-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1029
ID   ADE79530 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003130489-A1.
PD   10-JUL-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1030
ID   ADE75751 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003211571-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1031
ID   ADE73206 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003129592-A1.
PD   10-JUL-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1032
ID   ADE41296 standard; protein; 660 AA.
DE   Human secreted/transmembrane PRO polypeptide #23.
PN   US2003100497-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1033
ID   ADE23327 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003092108-A1.

PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADE23879 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003092110-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1035
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADE24522 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003092111-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 1036
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADD87347 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003203439-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 1037
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADE89213 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199062-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 1038
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADE41210 standard; protein; 660 AA.
DE   Human secreted/transmembrane polypeptide PRO265.
PN   US2003104558-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
RESULT 1039
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADE73741 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003148370-A1.
PD   07-AUG-2003.
PA   (GETH) GENENTECH INC.
RESULT 1040
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADE18352 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003194794-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 1041
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADE88661 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199054-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 1042
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADE99295 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003211576-A1.
PD   13-NOV-2003.

PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 1043
ID   ADE94681 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199027-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
RESULT 1044
ID   ADE91092 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199061-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 1045
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADE95233 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199052-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 1046
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADE93343 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199060-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 1047
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADF34924 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199029-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 1048
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADE98414 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003211569-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
RESULT 1049
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADE92239 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199051-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 1050
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADE90540 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199063-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 1051
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 1.1e-11;
ID   ADE91687 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003199058-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.

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Query Match          10.2%;    Score 320;   DB 8;   Length 660;
Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1052
ID   ADB98841 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003211568-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 1053
ID   ADG40311 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003225253-A1.
PD   04-DEC-2003.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.

Query Match          10.2%;    Score 320;   DB 8;   Length 660;
Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1054
ID   ADF73705 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003180312-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
RESULT 1055
ID   ADG02266 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207352-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 1056
ID   ADG22052 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207360-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.

Query Match          10.2%;    Score 320;   DB 8;   Length 660;
Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1057
ID   ADG20122 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207376-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 1058
ID   ADF98028 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207422-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 1059
ID   ADG24245 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207426-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.

Query Match          10.2%;    Score 320;   DB 8;   Length 660;
Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1060
ID   ADF98599 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003208055-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.

Query Match          10.2%;    Score 320;   DB 8;   Length 660;
Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1061
ID   ADG03430 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207351-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 1062
ID   ADF99151 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207353-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.

Query Match          10.2%;    Score 320;   DB 8;   Length 660;
Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1063
ID   ADG16736 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207355-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.

Query Match          10.2%;    Score 320;   DB 8;   Length 660;
Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1064
ID   ADG05195 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207375-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 1065
ID   ADG19462 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207425-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.

Query Match          10.2%;    Score 320;   DB 8;   Length 660;
Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1066
ID   ADF73281 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003166051-A1.
PD   04-SEP-2003.
PA   (GETH ) GENENTECH INC.

Query Match          10.2%;    Score 320;   DB 8;   Length 660;
Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1067
ID   ADG13299 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207357-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.

Query Match          10.2%;    Score 320;   DB 8;   Length 660;
Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1068
ID   ADG08356 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207424-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.

Query Match          10.2%;    Score 320;   DB 8;   Length 660;
Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1069
ID   ADG15526 standard; protein; 660 AA.
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DE   Human PRO polypeptide #175.
PN   US2003219985-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1070
ID   ADF96924 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207371-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1071
ID   ADG06109 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207374-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1072
ID   ADG23693 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207389-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1073
ID   ADG03982 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207423-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1074
ID   ADG24883 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207427-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1075
ID   ADG07180 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207350-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1076
ID   ADG07732 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207356-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1077
ID   ADG55227 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003194778-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1078
ID   ADG60891 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.

PN   US2003207390-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1079
ID   ADG61995 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207428-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1080
ID   ADG92124 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003027145-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1081
ID   ADG82196 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207358-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1082
ID   ADG57435 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207362-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1083
ID   ADG56883 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207364-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1084
ID   ADG55779 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207365-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1085
ID   ADG58519 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207368-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1086
ID   ADG70905 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207420-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 1.1e-11;
RESULT 1087
ID   ADG92551 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003027146-A1.
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PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1088
ID   ADG57987 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207363-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1089
ID   ADG53571 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207415-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1090
ID   ADG71457 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207421-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1091
ID   ADG81644 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207805-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1092
ID   ADH30606 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003077723-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1093
ID   ADG63645 standard; protein; 660 AA.
DE   Human secreted/transmembrane polypeptide PRO265.
PN   US2003180796-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1094
ID   ADH11973 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207419-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1095
ID   ADG52395 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207414-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1096
ID   ADG54123 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207416-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.

     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1097
ID   ADG81092 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003194793-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1098
ID   ADG56331 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207366-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1099
ID   ADH12597 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207378-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1100
ID   ADG61443 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207429-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1101
ID   ADH28530 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003022331-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1102
ID   ADG54675 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207367-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1103
ID   ADG59715 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207369-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1104
ID   ADH20340 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2004005553-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
     Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1105
ID   ADH43479 standard; protein; 660 AA.
DE   Human PRO polypeptide #23.
PN   US2003224984-A1.
PD   04-DEC-2003.
PA   (GETH ) GENENTECH INC.
     Query Match       10.2%;    Score 320;   DB 8;   Length 660;
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    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1106
ID  ADH07195 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2004006211-A1.
PD  08-JAN-2004.
PA  (DESN/) DESNOYERS L.
PA  (GODD/) GODDARD A.
PA  (GODO/) GODOWSKI P J.
PA  (GURN/) GURNEY A L.
PA  (MATH/) MATHER J P.
PA  (WILL/) WILLIAMS P M.
PA  (WOOD/) WOOD W I.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1107
ID  ADH59740 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003215904-A1.
PD  20-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1108
ID  ADH06768 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2004005665-A1.
PD  08-JAN-2004.
PA  (DESN/) DESNOYERS L.
PA  (GODD/) GODDARD A.
PA  (GODO/) GODOWSKI P J.
PA  (GURN/) GURNEY A L.
PA  (MATH/) MATHER J P.
PA  (WILL/) WILLIAMS P M.
PA  (WOOD/) WOOD W I.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1109
ID  ADI81139 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003207361-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1110
ID  ADI18510 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003152999-A1.
PD  14-AUG-2003.
PA  (GETH ) GENENTECH INC.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1111
ID  ADI65230 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003148419-A1.
PD  07-AUG-2003.
PA  (GETH ) GENENTECH INC.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1112
ID  ADI37493 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003096340-A1.
PD  22-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1113
ID  ADG09882 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2004009548-A1.

PD  15-JAN-2004.
PA  (GETH ) GENENTECH INC.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1114
ID  ADH97297 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003190610-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1115
ID  ADI15353 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003207382-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1116
ID  ADG09230 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2004009547-A1.
PD  15-JAN-2004.
PA  (GETH ) GENENTECH INC.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1117
ID  ADI14685 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003207383-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1118
ID  ADH60400 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2004023331-A1.
PD  05-FEB-2004.
PA  (DESN/) DESNOYERS L.
PA  (GODD/) GODDARD A.
PA  (GODO/) GODOWSKI P J.
PA  (GURN/) GURNEY A L.
PA  (MATH/) MATHER J P.
PA  (WILL/) WILLIAMS P M.
PA  (WOOD/) WOOD W I.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1119
ID  ADI18280 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003187238-A1.
PD  02-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1120
ID  ADJ99457 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003187238-A1.
PD  02-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
    Best Local Similarity    22.4%;    Pred. No. 1.1e-11;
RESULT 1121
ID  ADL08650 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003186358-A1.
PD  02-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match              10.2%;    Score 320;  DB 8;  Length 660;
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     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1122
ID   ADM24995 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003096233-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660
     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1123
ID   ADJ63561 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2004039164-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660
     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1124
ID   ADM29741 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003190611-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660
     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1125
ID   ADJ77456 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2004038336-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660
     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1126
ID   ADK82824 standard; protein; 660 AA.
DE   Human PRO polypeptide #23.
PN   US2004043927-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660
     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1127
ID   ADJ65578 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2004038335-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660
     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1128
ID   ADM27714 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2004048333-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660
     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1129
ID   ADM42438 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2004058424-A1.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660
     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1130
ID   ADO06063 standard; protein; 660 AA.
DE   Human PRO polypeptide #6.
PN   US6686451-B1.
PD   03-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660
     Best Local Similarity 22.4%;

RESULT 1131
ID   ADM28300 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2004007064-A1.
PD   22-APR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660;
     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1132
ID   ADR10915 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2004137561-A1.
PD   15-JUL-2004.
PA   (GETH ) GENENTECH INC.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660;
     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1133
ID   ADR17824 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2004147017-A1.
PD   29-JUL-2004.
PA   (ASHK/)  ASHKENAZI A.
PA   (BOTS/)  BOTSTEIN D.
PA   (DESN/)  DESNOYERS L.
PA   (EATO/)  EATON D L.
PA   (FERR/)  FERRARA N.
PA   (FILV/)  FILVAROFF E.
PA   (FONG/)  FONG S.
PA   (GAOW/)  GAO W.
PA   (GERB/)  GERBER H.
PA   (GERR/)  GERRITSEN M E.
PA   (GODD/)  GODDARD A.
PA   (GODO/)  GODOWSKI P J.
PA   (GRIM/)  GRIMALDI C J.
PA   (GURN/)  GURNEY A L.
PA   (HILL/)  HILLAN K J.
PA   (KLJA/)  KLJAVIN I J.
PA   (MATH/)  MATHER J P.
PA   (PANJ/)  PAN J.
PA   (PAON/)  PAONI N F.
PA   (ROYM/)  ROY M A.
PA   (STEW/)  STEWART T A.
PA   (TUMA/)  TUMAS D.
PA   (WILL/)  WILLIAMS P M.
PA   (WOOD/)  WOOD W I.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660;
     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1134
ID   ADI95782 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003077659-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660;
     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1135
ID   ADI96634 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207354-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660;
     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1136
ID   ADI65657 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003148371-A1.
PD   07-AUG-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.2%;    Score 320;  DB 8;  Length 660;
     Best Local Similarity 22.4%;    Pred. No. 1.1e-11;
RESULT 1137
ID   ADS74463 standard; protein; 660 AA.
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DE   Human secreted/transmembrane protein #7.
PN   US200418531-A1.
PD   23-SEP-2004.
PA   (ASHK/) ASHKENAZI A.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI C J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (MATH/) MATHER J P.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Query Match        10.2%;    Score 320;  DB 8;  Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1138
ID   ADS32286 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US200420125-A1.
PD   14-OCT-2004.
PA   (GETH ) GENENTECH INC.
Query Match        10.2%;    Score 320;  DB 8;  Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1139
ID   ADT03270 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US200421426-A1.
PD   28-OCT-2004.
PA   (GETH ) GENENTECH INC.
Query Match        10.2%;    Score 320;  DB 8;  Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1140
ID   ADT03500 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US200315292-A1.
PD   14-AUG-2003.
PA   (GETH ) GENENTECH INC.
Query Match        10.2%;    Score 320;  DB 8;  Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1141
ID   ADU06386 standard; protein; 660 AA.
DE   Novel bronchial cancer-associated human protein SeqID610.
PN   DE10316701-A1.
PD   04-NOV-2004.
PA   (HINZ/) HINZMANN B.
PA   (HERM/) HERMANN K.
PA   (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match        10.2%;    Score 320;  DB 8;  Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1142
ID   ADZ03321 standard; protein; 660 AA.
DE   Human secreted/transmembrane PRO265 protein.
PN   US200507487-A1.
PD   07-APR-2005.
PA   (GETH ) GENENTECH INC.
Query Match        10.2%;    Score 320;  DB 9;  Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1143
ID   AEA37738 standard; protein; 660 AA.

DE   Human secreted/transmembrane protein, #7.
PN   US2005112725-A1.
PD   26-MAY-2005.
PA   (GETH ) GENENTECH INC.
Query Match        10.2%;    Score 320;  DB 9;  Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1144
ID   AEB14067 standard; protein; 660 AA.
DE   Cancer cell diagnosis method-related human protein - SEQ ID 350.
PN   US2005153396-A1.
PD   14-JUL-2005.
PA   (BAKE/) BAKER K P.
PA   (BERE/) BERESINI M.
PA   (DEFO/) DEFORGE L.
PA   (DESN/) DESNOYERS L.
PA   (FILV/) FILVAROFF E.
PA   (GAOW/) GAO W.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (SHER/) SHERWOOD S.
PA   (SMIT/) SMITH V.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W I.
PA   (ZHAN/) ZHANG Z.
Query Match        10.2%;    Score 320;  DB 9;  Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1145
ID   AED23772 standard; protein; 660 AA.
DE   Human secreted protein PRO 265, SEQ ID 28.
PN   US200514904-A1.
PD   29-SEP-2005.
PA   (GETH ) GENENTECH INC.
Query Match        10.2%;    Score 320;  DB 9;  Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1146
ID   AED86265 standard; protein; 660 AA.
DE   Human PRO amino acid sequence, seq id 350.
PN   US2005245730-A1.
PD   03-NOV-2005.
PA   (GETH ) GENENTECH INC.
Query Match        10.2%;    Score 320;  DB 9;  Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1147
ID   AEE68941 standard; protein; 660 AA.
DE   Fibromodulin homologous PRO265 protein, SEQ ID 28.
PN   US6974689-B1.
PD   13-DEC-2005.
PA   (GETH ) GENENTECH INC.
Query Match        10.2%;    Score 320;  DB 10;  Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1148
ID   AEG58212 standard; protein; 660 AA.
DE   Human PRO265 polypeptide SEQ ID NO: 350.
PN   US2006073568-A1.
PD   06-APR-2006.
PA   (GETH ) GENENTECH INC.
Query Match        10.2%;    Score 320;  DB 10;  Length 660;
Best Local Similarity 22.4%; Pred. No. 1.1e-11;
RESULT 1149
ID   ABI43857 standard; protein; 660 AA.
DE   Human cancer-related PRO protein amino acid sequence - SEQ ID 350.
PN   US2006040351-A1.
PD   23-FEB-2006.
PA   (BAKE/) BAKER K P.
PA   (BERE/) BERESINI M.
PA   (DEFO/) DEFORGE L.
PA   (DESN/) DESNOYERS L.
PA   (FILV/) FILVAROFF E.
PA   (GAOW/) GAO W.
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PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
  Query Match   10.2%;   Score 320; DB 10; Length 660;
  Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1150
ID AEI23940 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265, SEQ ID NO:350.
PN EP1672070-A2.
PD 21-JUN-2006.
PA (GETH) GENENTECH INC.
  Query Match   10.2%;   Score 320; DB 10; Length 660;
  Best Local Similarity 22.4%;   Pred. No. 1.1e-11;
RESULT 1151
ID ADT77808 standard; protein; 452 AA.
DE Chimeric Nogo receptor polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP) UNIV ROCHESTER.
  Query Match   10.2%;   Score 318.5; DB 8; Length 452;
  Best Local Similarity 27.8%;   Pred. No. 8.4e-12;
RESULT 1152
ID ADT77802 standard; protein; 452 AA.
DE Chimeric Nogo receptor polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP) UNIV ROCHESTER.
  Query Match   10.2%;   Score 318.5; DB 8; Length 452;
  Best Local Similarity 27.8%;   Pred. No. 8.4e-12;
RESULT 1153
ID AEF79023 standard; protein; 648 AA.
DE Mouse NAG14 polypeptide SEQ ID NO: 6.
PN US2006035826-A1.
PD 16-FEB-2006.
PA (LINJ/) LIN J C.
PA (ROSE/) ROSENTHAL A.
  Query Match   10.1%;   Score 317.5; DB 10; Length 648;
  Best Local Similarity 25.0%;   Pred. No. 1.5e-11;
RESULT 1154
ID AAB13006 standard; protein; 713 AA.
DE Human leucine-rich repeat (LRR) family member protein.
PN WO200175105-A2.
PD 11-OCT-2001.
PA (MILL-) MILLENNIUM PHARM INC.
  Query Match   10.1%;   Score 317.5; DB 4; Length 713;
  Best Local Similarity 23.1%;   Pred. No. 1.7e-11;
RESULT 1155
ID AAU91335 standard; protein; 713 AA.
DE Human novel secreted protein LP223(a).
PN WO20021435B-A2.
PD 21-FEB-2002.
PA (ELIL) LILLY & CO ELI.
  Query Match   10.1%;   Score 316.5; DB.5; Length 713;
  Best Local Similarity 23.1%;   Pred. No. 1.9e-11;
RESULT 1156
ID ABG97991 standard; protein; 713 AA.
DE Human nervous system leucine rich repeat protein (HLRRNS1) #2.
PN WO20274959-A2.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
  Query Match   10.1%;   Score 316.5; DB 5; Length 713;
  Best Local Similarity 23.1%;   Pred. No. 1.9e-11;
RESULT 1157
ID ABU52381 standard; protein; 713 AA.
DE Human GPCR related protein NOV31a.

PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
  Query Match   10.1%;   Score 316.5; DB 6; Length 713;
  Best Local Similarity 23.1%;   Pred. No. 1.9e-11;
RESULT 1158
ID ABI93171 standard; protein; 713 AA.
DE Novel human secreted protein, LP223(a).
PN US2006147945-A1.
PD 06-JUL-2006.
PA (EDMO/) EDMONDS B T.
PA (MICA/) MICANOVIC R.
PA (OUWW/) OU W.
PA (SUEW/) SU E W.
PA (TSCH/) TSCHANG S R.
PA (WANG/) WANG H.
  Query Match   10.1%;   Score 316.5; DB 10; Length 713;
  Best Local Similarity 23.1%;   Pred. No. 1.9e-11;
RESULT 1159
ID ADT77796 standard; protein; 474 AA.
DE Chimeric Nogo receptor polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP) UNIV ROCHESTER.
  Query Match   10.0%;   Score 314.5; DB 8; Length 474;
  Best Local Similarity 27.8%;   Pred. No. 1.6e-11;
RESULT 1160
ID AAU91341 standard; protein; 656 AA.
DE Human novel secreted protein LP223(b).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL) LILLY & CO ELI.
  Query Match   10.0%;   Score 313.5; DB 5; Length 656;
  Best Local Similarity 23.6%;   Pred. No. 2.7e-11;
RESULT 1161
ID ABI93183 standard; protein; 656 AA.
DE Novel human secreted protein, LP223(b).
PN US2006147945-A1.
PD 06-JUL-2006.
PA (EDMO/) EDMONDS B T.
PA (MICA/) MICANOVIC R.
PA (OUWW/) OU W.
PA (SUEW/) SU E W.
PA (TSCH/) TSCHANG S R.
PA (WANG/) WANG H.
  Query Match   10.0%;   Score 313.5; DB 10; Length 656;
  Best Local Similarity 23.6%;   Pred. No. 2.7e-11;
RESULT 1162
ID ADL24097 standard; protein; 713 AA.
DE Human NOVX polypeptide #71.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) KEKUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S G.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.
PA (CASM/) CASMAN S J.
PA (PENA/) PENA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.

PA   (ZERH/) ZERHUSEN B D.
PA   (GERL/) GERLACH V.
PA   (POCH/) POCHART P F.
PA   (FERN/) FERNANDES E R.
PA   (SHIM/) SHIMKETS R A.
PA   (RAST/) RASTELLI L.
PA   (SPAD/) SPADERNA S K.
PA   (LARO/) LAROCHELLE W J.
PA   (ZHON/) ZHONG M.
PA   (KHRA/) KHRAMTSOV N V.
PA   (VOSS/) VOSS E Z.
PA   (HERR/) HERRMANN J L.
      Query Match   10.0%;   Score 313.5; DB 8; Length 713;
      Best Local Similarity 23.1%;   Pred. No. 3e-11;
RESULT 1163
ID AAE09437 standard; protein; 592 AA.
DE Human sbgTango79a protein.
PN WO200016050-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
      Query Match   10.0%;   Score 312; DB 4; Length 592;
      Best Local Similarity 25.9%;   Pred. No. 3e-11;
RESULT 1164
ID AAE25351 standard; protein; 592 AA.
DE Human LP polypeptide, LP243.
PN WO200248361-A2.
PD 20-JUN-2002.
PA (ELIL) LILLY & CO ELI.
      Query Match   10.0%;   Score 312; DB 5; Length 592;
      Best Local Similarity 25.9%;   Pred. No. 3e-11;
RESULT 1165
ID AAU91329 standard; protein; 592 AA.
DE Human novel secreted protein LP243(b).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL) LILLY & CO ELI.
      Query Match   10.0%;   Score 312; DB 5; Length 592;
      Best Local Similarity 25.9%;   Pred. No. 3e-11;
RESULT 1166
ID ABP60996 standard; protein; 592 AA.
DE Novel human protein. SEQ ID 83.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
      Query Match   10.0%;   Score 312; DB 5; Length 592;
      Best Local Similarity 25.9%;   Pred. No. 3e-11;
RESULT 1167
ID AAU79167 standard; protein; 592 AA.
DE Human leucine-rich repeat proteins-like protein NOV4.
PN WO200214368-A2.
PD 21-FEB-2002.
PA (CURA-) CURAGEN CORP.
      Query Match   10.0%;   Score 312; DB 6; Length 592;
      Best Local Similarity 25.9%;   Pred. No. 3e-11;
RESULT 1168
ID ABG74693 standard; protein; 592 AA.
DE Human CGDD protein 6803363CD1 SEQ ID 19.
PN WO200314322-A2.
PD 20-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
      Query Match   10.0%;   Score 312; DB 6; Length 592;
      Best Local Similarity 25.9%;   Pred. No. 3e-11;
RESULT 1169
ID ADE03417 standard; protein; 592 AA.
DE Human immunoglobulin superfamily member BGS-2.
PN US2003195163-A1.
PD 16-OCT-2003.
PA (WUSS/) WU S.
PA (KRYS/) KRYSTEK S R.
PA (LEEL/) LEE L.

PA   (FEDE/) FEDER J N.
PA   (CHEN/) CHENG J D.
      Query Match   10.0%;   Score 312; DB 7; Length 592;
      Best Local Similarity 25.9%;   Pred. No. 3e-11;
RESULT 1170
ID ADU02709 standard; protein; 592 AA.
DE Novel human polypeptide seqid 1176.
PN WO2004093804-A2.
PD 04-NOV-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
      Query Match   10.0%;   Score 312; DB 8; Length 592;
      Best Local Similarity 25.9%;   Pred. No. 3e-11;
RESULT 1171
ID AEI93159 standard; protein; 592 AA.
DE Novel human secreted protein, LP243(b).
PN US2006147945-A1.
PD 06-JUL-2006.
PA (EDMO/) EDMONDS B T.
PA (MICA/) MICANOVIC R.
PA (OUWW/) OU W.
PA (SUEW/) SU E W.
PA (TSCH/) TSCHANG S R.
PA (WANG/) WANG H.
      Query Match   10.0%;   Score 312; DB 10; Length 592;
      Best Local Similarity 25.9%;   Pred. No. 3e-11;
RESULT 1172
ID ABG61770 standard; protein; 608 AA.
DE Novel leucine-rich protein.
PN WO200229058-A2.
PD 11-APR-2002.
PA (CURA-) CURAGEN CORP.
      Query Match   10.0%;   Score 312; DB 5; Length 608;
      Best Local Similarity 25.9%;   Pred. No. 3.1e-11;
RESULT 1173
ID ABG97967 standard; protein; 634 AA.
DE Human nervous system leucine rich repeat protein (HLRRNS1) #1.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
      Query Match   9.9%;   Score 311; DB 5; Length 634;
      Best Local Similarity 24.1%;   Pred. No. 3.7e-11;
RESULT 1174
ID ABR55628 standard; protein; 420 AA.
DE Amino acid sequence of rat Nogo-66 receptor homologue NgRH1.
PN WO200303687-A1.
PD 01-MAY-2003.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
      Query Match   9.9%;   Score 310.5; DB 6; Length 420;
      Best Local Similarity 29.8%;   Pred. No. 2.5e-11;
RESULT 1175
ID ADT77788 standard; protein; 420 AA.
DE Rat Nogo receptor 2 polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP) UNIV ROCHESTER.
      Query Match   9.9%;   Score 310.5; DB 8; Length 420;
      Best Local Similarity 29.8%;   Pred. No. 2.5e-11;
RESULT 1176
ID AAO23115 standard; protein; 674 AA.
DE FLRT1 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
      Query Match   9.9%;   Score 310.5; DB 6; Length 674;
      Best Local Similarity 21.5%;   Pred. No. 4.3e-11;
RESULT 1177
ID ADH17606 standard; protein; 674 AA.
DE Human NOV19a protein - SEQ ID 296.
PN WO2003093433-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
      Query Match   9.9%;   Score 310.5; DB 8; Length 674;

Best Local Similarity   21.5%;   Pred. No. 4.3e-11;
RESULT 1178
ID   ADH17628 standard; protein; 674 AA.
DE   Human NOV19l protein - SEQ ID 318.
PN   WO2003093432-A2.
PD   13-NOV-2003.
PA   (CURA-) CURAGEN CORP.   9.9%;   Score 310.5; DB 8;   Length 674;
     Query Match
     Best Local Similarity   21.5%;   Pred. No. 4.3e-11;
RESULT 1179
ID   ADH17630 standard; protein; 674 AA.
DE   Human NOV19m protein - SEQ ID 320.
PN   WO2003093432-A2.
PD   13-NOV-2003.
PA   (CURA-) CURAGEN CORP.   9.9%;   Score 310.5; DB 8;   Length 674;
     Best Local Similarity   21.5%;   Pred. No. 4.3e-11;
RESULT 1180
ID   ADH17634 standard; protein; 674 AA.
DE   Human NOV19o protein - SEQ ID 324.
PN   WO2003093432-A2.
PD   13-NOV-2003.
PA   (CURA-) CURAGEN CORP.   9.9%;   Score 310.5; DB 8;   Length 674;
     Best Local Similarity   21.5%;   Pred. No. 4.3e-11;
RESULT 1181
ID   ADH17632 standard; protein; 674 AA.
DE   Human NOV19n protein - SEQ ID 322.
PN   WO2003093432-A2.
PD   13-NOV-2003.
PA   (CURA-) CURAGEN CORP.   9.9%;   Score 310.5; DB 8;   Length 674;
     Query Match
     Best Local Similarity   21.5%;   Pred. No. 4.3e-11;
RESULT 1182
ID   AB027346 standard; protein; 585 AA.
DE   Human secreted/transmembrane polypeptide PRO1865.
PN   US2003009012-A1.
PD   09-JAN-2003.
PA   (GETH) GENENTECH INC.   9.9%;   Score 309; DB 6;   Length 585;
     Query Match
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1183
ID   AB034232 standard; protein; 585 AA.
DE   Human secreted/transmembrane polypeptide PRO 1865.
PN   US2003060601-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.   9.9%;   Score 309; DB 6;   Length 585;
     Query Match
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1184
ID   AAU29215 standard; protein; 649 AA.
DE   Human PRO polypeptide sequence #192.
PN   WO20016848-A2.
PD   20-SEP-2001.
PA   (GETH) GENENTECH INC.   9.9%;   Score 309; DB 4;   Length 649;
     Query Match
     Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1185
ID   AAB70533 standard; protein; 649 AA.
DE   Human PRO3 protein sequence SEQ ID NO:6.
PN   WO200110902-A2.
PD   15-FEB-2001.
PA   (CURA-) CURAGEN CORP.   9.9%;   Score 309; DB 4;   Length 649;
     Query Match
     Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1186
ID   AAB87591 standard; protein; 649 AA.
DE   Human PRO1865.
PN   WO20011631B-A2.
PD   08-MAR-2001.
PA   (GETH) GENENTECH INC.   9.9%;   Score 309; DB 4;   Length 649;
     Query Match
     Best Local Similarity   22.3%;   Pred. No. 5.2e-11;

RESULT 1187
ID   ABG95916 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein PRO1865.
PN   US2002119130-A1.
PD   29-AUG-2002.
PA   (GETH) GENENTECH INC.   9.9%;   Score 309; DB 5;   Length 649;
     Query Match
     Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1188
ID   ABB84953 standard; protein; 649 AA.
DE   Human PRO1865 protein sequence SEQ ID NO:274.
PN   WO200200690-A2.
PD   03-JAN-2002.
PA   (GETH) GENENTECH INC.   9.9%;   Score 309; DB 5;   Length 649;
     Query Match
     Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1189
ID   ABP70109 standard; protein; 649 AA.
DE   Human NOV27a.
PN   WO200272771-A2.
PD   19-SEP-2002.
PA   (CURA-) CURAGEN CORP.   9.9%;   Score 309; DB 5;   Length 649;
     Query Match
     Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1190
ID   ABB95559 standard; protein; 649 AA.
DE   Human angiogenesis related protein PRO1865 SEQ ID NO: 274.
PN   WO200208284-A2.
PD   31-JAN-2002.
PA   (GETH) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
     Query Match   9.9%;   Score 309; DB 5;   Length 649;
     Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1191
ID   ABU58591 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US200302272-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.   9.9%;   Score 309; DB 6;   Length 649;
     Query Match
     Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1192
ID   ABU88139 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003033127-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.   9.9%;   Score 309; DB 6;   Length 649;
     Query Match
     Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1193
ID   ABU84454 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032112-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.   9.9%;   Score 309; DB 6;   Length 649;
     Query Match
     Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1194
ID   ABR66328 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027278-A1.
PD   06-FEB-2003.

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       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1195
ID   ABR65718 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003036159-A1.
PD   20-FEB-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1196
ID   ABU99658 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003040070-A1.
PD   27-FEB-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1197
ID   ABU82897 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032113-A1.
PD   13-FEB-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1198
ID   ABU90018 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036147-A1.
PD   20-FEB-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1199
ID   ABR68267 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027264-A1.
PD   06-FEB-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1200
ID   ABU96320 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036144-A1.
PD   20-FEB-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1201
ID   ABU92751 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036149-A1.
PD   20-FEB-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1202
ID   ABO08828 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003044923-A1.
PD   06-MAR-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1203
ID   ABO02880 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003040062-A1.
PD   27-FEB-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1204
ID   ABR75034 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040056-A1.
PD   27-FEB-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1205


ID   ABR94796 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003044926-A1.
PD   06-MAR-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1206
ID   ABU85769 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003036140-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1207
ID   ABU98929 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003013153-A1.
PD   16-JAN-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1208
ID   ABU98144 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003017544-A1.
PD   23-JAN-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1209
ID   ABU91850 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003027277-A1.
PD   06-FEB-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1210
ID   ABU89543 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003036141-A1.
PD   20-FEB-2003.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1211
ID   ABU86384 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036146-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1212
ID   ABU67597 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036162-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1213
ID   ABU80625 standard; protein; 649 AA.
DE   Human PRO protein #192.
PN   US2003036137-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
       Best Local Similarity         22.3%;    Pred. No. 5.2e-11;
RESULT 1214
ID   ABU90941 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003018173-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.

       Query Match                    9.9%;    Score 309;    DB 6;    Length 649;
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          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1215
ID   ABO34000 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein PRO1865.
PN   US2003009013-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1216
ID   ABR99543 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040063-A1.
PD   27-FEB-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1217
ID   ABR99933 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040064-A1.
PD   27-FEB-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1218
ID   ABO16456 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003027267-A1.
PD   06-FEB-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1219
ID   ABR92356 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003036160-A1.
PD   20-FEB-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1220
ID   ABO18997 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003044925-A1.
PD   06-MAR-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1221
ID   ABR78418 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054474-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1222
ID   ABU72017 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003018183-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1223
ID   ABU85154 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003032114-A1.
PD   13-FEB-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1224
ID   ABO00293 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003032101-A1.
PD   13-FEB-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;


          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1225
ID   ABO11625 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036124-A1.
PD   20-FEB-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1226
ID   ABO02270 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003040054-A1.
PD   27-FEB-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1227
ID   ABU88844 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036133-A1.
PD   20-FEB-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1228
ID   ABU83539 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036134-A1.
PD   20-FEB-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1229
ID   ABO06340 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003022294-A1.
PD   30-JAN-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1230
ID   ABR59376 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027275-A1.
PD   06-FEB-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1231
ID   ABO09938 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003027324-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1232
ID   ABO19302 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036118-A1.
PD   20-FEB-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1233
ID   ABO11320 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036123-A1.
PD   20-FEB-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1234
ID   ABR66938 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003036148-A1.
PD   20-FEB-2003.
     Query Match    9.9%;   Score 309; DB 6;   Length 649;
          Best Local Similarity   22.3%;   Pred. No. 5.2e-11;
RESULT 1235
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ID   ABO16151 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003040060-A1.
PD   27-FEB-2003.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1236
ID   ABO13857 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003044916-A1.
PD   06-MAR-2003.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1237
ID   ABU71571 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865.
PN   US2003013855-A1.
PD   16-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1238
ID   ABU65760 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein, SEQ ID 384.
PN   US2003036156-A1.
PD   20-FEB-2003.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1239
ID   ABO07608 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032117-A1.
PD   13-FEB-2003.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1240
ID   ABO03795 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036128-A1.
PD   20-FEB-2003.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1241
ID   ABR67243 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027266-A1.
PD   06-FEB-2003.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1242
ID   ABO15846 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003054483-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1243
ID   ABU56127 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein, PRO1865.
PN   US2003022298-A1.
PD   30-JAN-2003.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1244
ID   ABU72352 standard; protein; 649 AA.
DE   Human PRO polypeptide #66.
PN   US2002218638-A1.
PD   05-DEC-2002.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1245

ID   ABU65455 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032102-A1.
PD   13-FEB-2003.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1246
ID   ABU95400 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036117-A1.
PD   20-FEB-2003.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1247
ID   ABU71303 standard; protein; 649 AA.
DE   Human PRO1865 protein.
PN   US2003036143-A1.
PD   20-FEB-2003.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1248
ID   ABO07913 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032130-A1.
PD   13-FEB-2003.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1249
ID   ABR70154 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032118-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1250
ID   ABR69487 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003036132-A1.
PD   20-FEB-2003.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1251
ID   ABO01628 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003008353-A1.
PD   09-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1252
ID   ABU81430 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003017542-A1.
PD   23-JAN-2003.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1253
ID   ABR60227 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032137-A1.
PD   13-FEB-2003.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1254
ID   ABU91025 standard; protein; 649 AA.
DE   Human PRO polypeptide #66.
PN   US2003018168-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1255

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ID   ABR67962 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027269-A1.
PD   06-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1256
ID   ABR65350 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027268-A1.
PD   06-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1257
ID   ABR68572 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027274-A1.
PD   06-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1258
ID   ABR71984 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032135-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1259
ID   ABU85464 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003022295-A1.
PD   30-JAN-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1260
ID   ABU89154 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003022297-A1.
PD   30-JAN-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1261
ID   ABU83234 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032105-A1.
PD   13-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1262
ID   ABU95090 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003032123-A1.
PD   13-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1263
ID   ABU90638 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003032108-A1.
PD   13-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1264
ID   ABU84149 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032111-A1.
PD   13-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1265
ID   ABU93800 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.

PN   US2003032119-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1266
ID   ABR65045 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027263-A1.
PD   06-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1267
ID   ABR68877 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027271-A1.
PD   06-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1268
ID   ABO06693 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036125-A1.
PD   20-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1269
ID   ABR99238 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040068-A1.
PD   27-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1270
ID   ABU57122 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003027280-A1.
PD   06-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1271
ID   ABU86074 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003022300-A1.
PD   30-JAN-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1272
ID   ABU82361 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036136-A1.
PD   20-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1273
ID   ABU87372 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003036138-A1.
PD   20-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1274
ID   ABU83844 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032109-A1.
PD   13-FEB-2003.
     Query Match          9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1275
ID   ABO08218 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003040066-A1.
PD   27-FEB-2003.
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          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1276
ID   ABU92541 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein PRO1865.
PN   US2003045684-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1277
ID   ABU81929 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003032104-A1.
PD   13-FEB-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1278
ID   ABU66093 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036157-A1.
PD   20-FEB-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1279
ID   ABU81211 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865.
PN   US2003027212-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1280
ID   ABR59922 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032120-A1.
PD   13-FEB-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1281
ID   ABU94110 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036155-A1.
PD   20-FEB-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1282
ID   ABU99963 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003022296-A1.
PD   30-JAN-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1283
ID   ABR66633 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027281-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1284
ID   ABR91051 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040058-A1.
PD   27-FEB-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1285
ID   ABO53325 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003027986-A1.
PD   06-FEB-2003.

PA   (GETH ) GENENTECH INC.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1286
ID   ABU94478 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003017540-A1.
PD   23-JAN-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1287
ID   ABU79360 standard; protein; 649 AA.
DE   Human PRO polypeptide #192
PN   US2003032106-A1.
PD   13-FEB-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1288
ID   ABU86689 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032129-A1.
PD   13-FEB-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1289
ID   ABU86994 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003032131-A1.
PD   13-FEB-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1290
ID   ABU94783 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032103-A1.
PD   13-FEB-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1291
ID   ABO04710 standard; protein; 649 AA.
DE   Human PRO polypeptide #192
PN   US2003032107-A1.
PD   13-FEB-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1292
ID   ABR70459 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032139-A1.
PD   13-FEB-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1293
ID   ABU98624 standard; protein; 649 AA.
DE   Human PRO polypeptide #192
PN   US2003022301-A1.
PD   30-JAN-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1294
ID   ABR66023 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003036165-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%; Score 309; DB 6; Length 649;
          Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1295
ID   ABR64740 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027262-A1.
PD   06-FEB-2003.
          Query Match          9.9%; Score 309; DB 6; Length 649;
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Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1296
ID   ABU79665 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032110-A1.
PD   13-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1297
ID   ABU93056 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036142-A1.
PD   20-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1298
ID   ABU96015 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003036145-A1.
PD   20-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1299
ID   ABU91235 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036154-A1.
PD   20-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1300
ID   ABU90328 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036153-A1.
PD   20-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1301
ID   ABO09743 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003044931-A1.
PD   06-MAR-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1302
ID   ABO11015 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2002183493-A1.
PD   05-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1303
ID   ABR71069 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040069-A1.
PD   27-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1304
ID   ABU98328 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2002183493-A1.
PD   05-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1305
ID   ABU87677 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003022293-A1.
PD   30-JAN-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1306

ID   ABU91545 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032128-A1.
PD   13-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1307
ID   ABU89333 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036634-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1308
ID   ABU84759 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032116-A1.
PD   13-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1309
ID   ABR69849 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032122-A1.
PD   13-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1310
ID   ABU80226 standard; protein; 649 AA.
DE   Human PRO protein #192.
PN   US2003036139-A1.
PD   20-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1311
ID   ABU82540 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2002183494-A1.
PD   05-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1312
ID   ABU93495 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003017541-A1.
PD   23-JAN-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1313
ID   ABO10048 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003017543-A1.
PD   23-JAN-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1314
ID   ABO09133 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036152-A1.
PD   20-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1315
ID   ABU95504 standard; protein; 649 AA.
DE   Human PRO polypeptide #66.
PN   US2003027993-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%;   Pred. No. 5.2e-11;
RESULT 1316

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ID   ABU10701 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein #192.
PN   US2002127584-A1.
PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1317
ID   ABU72174 standard; protein; 649 AA.
DE   Human PRO polypeptide #66.
PN   US2003023042-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1318
ID   ABU95710 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032115-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1319
ID   ABU96919 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003032140-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1320
ID   ABR70764 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040076-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1321
ID   ABO05115 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003008352-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1322
ID   ABO08523 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003044922-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1323
ID   ABO05730 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032118-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1324
ID   ABR74119 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003036135-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1325
ID   ABR95711 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054455-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1326
ID   ABR81008 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049741-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1327
ID   ABR81313 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049743-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1328
ID   ABM01009 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049769-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1329
ID   ABR88611 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068743-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1330
ID   ABM77432 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054479-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1331
ID   ABO28916 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068685-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1332
ID   ABO31661 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068725-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1333
ID   ABM08078 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068752-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1334
ID   ABO40558 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068682-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
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RESULT 1335
ID   ABO35983 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003068701-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1336
ID   ABO44122 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003068755-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1337
ID   ADA78136 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003073180-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1338
ID   ABM24917 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104539-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1339
ID   ABO03185 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036131-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1340
ID   ABR90441 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040075-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1341
ID   ABM17355 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054459-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1342
ID   ABR95101 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003044930-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1343
ID   ABR95406 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040071-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1344
ID   ADB17189 standard; protein; 649 AA.
DE   Human transmembrane PRO polypeptide (SeqID 132).
PN   US2003050462-A1.
PD   13-MAR-2003.

PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1345
ID   ABO21644 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003054471-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1346
ID   ABR97908 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064452-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1347
ID   ABR87696 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068705-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1348
ID   ABM77737 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054473-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1349
ID   ABM27967 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064440-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1350
ID   ABM06248 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068704-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1351
ID   ABM03754 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068722-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1352
ID   ABM35205 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003073183-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1353
ID   ABM26442 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104549-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
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          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1354
ID   ABO48224 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003049749-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1355
ID   ABR92966 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064462-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1356
ID   ABO24727 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003065159-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1357
ID   ABM11738 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064447-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1358
ID   ABM02839 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003073184-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1359
ID   ABM16135 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064463-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1360
ID   ABO27696 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003064451-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1361
ID   ABM29187 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068721-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1362
ID   ABM07163 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003066699-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;

RESULT 1363
ID   ABM21257 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068707-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1364
ID   ABM09603 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003073175-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1365
ID   ABO41473 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068695-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1366
ID   ABO36288 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003068703-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1367
ID   ABO43817 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003068732-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1368
ID   ABM76517 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003082717-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1369
ID   ABM76213 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104548-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1370
ID   ABM25832 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104542-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1371
ID   ABM26137 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104543-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
          Query Match        9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1372
ID   ABO03490 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036127-A1.
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PD   20-FEB-2003.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1373
ID   ABO02575 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003040061-A1.
PD   27-FEB-2003.
RESULT 1374
ID   ABO44304 standard; protein; 649 AA.
DE   Human secreted/transmembrane polypeptide PRO 1865.
PN   US2003018172-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1375
ID   ABR90746 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003036130-A1.
PD   20-FEB-2003.
RESULT 1376
ID   ABR73814 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054468-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1377
ID   ABO17066 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003054470-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1378
ID   ABR94491 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003044917-A1.
PD   06-MAR-2003.
RESULT 1379
ID   ABR75998 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003044929-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1380
ID   ABR71374 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003059880-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1381
ID   ABR93271 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064465-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1382
ID   ABR93576 standard; protein; 649 AA.

DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054478-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1383
ID   ABR88001 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068718-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1384
ID   ABO28001 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003064454-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1385
ID   ABO30136 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003064461-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1386
ID   ABO33345 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003068724-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1387
ID   ABM05033 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068727-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1388
ID   ABM08993 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068772-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1389
ID   ABO35593 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068714-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1390
ID   ABO35678 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003068758-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        9.9%;  Score 309; DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
RESULT 1391
ID   ABO39643 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
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PN   US2003068776-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1392
ID   ABM10518 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003069407-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1393
ID   ABM12043 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104555-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1394
ID   ABO52189 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003049768-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1395
ID   ABO52494 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003049771-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1396
ID   ADA19994 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003069394-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1397
ID   ABO23812 standard; protein; 649 AA.
DE   Human secreted/transmembrane PRO polypeptide (PRO) #192.
PN   US2003032134-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1398
ID   ADB17377 standard; protein; 649 AA.
DE   Human transmembrane PRO polypeptide (SeqID 132).
PN   US2003050465-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1399
ID   ABR97298 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054481-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1400
ID   ABR87086 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049778-A1.
PD   13-MAR-2003.
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PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1401
ID   ABM11128 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049782-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1402
ID   ABM28272 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054476-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1403
ID   ABO32271 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068733-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1404
ID   ABM15398 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068692-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1405
ID   ABM06553 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068709-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1406
ID   ABM04364 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068716-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1407
ID   ABM22477 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068740-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1408
ID   ABM07773 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068751-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1409
ID   ABO40863 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068684-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
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          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1410
ID   ABM35510 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003073179-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1411
ID   ABM33273 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003087374-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1412
ID   ABO52799 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003049773-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1413
ID   ABO50359 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003049777-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1414
ID   ABU09353 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003040055-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1415
ID   ABO04405 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003035164-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1416
ID   ABO06035 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003040074-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1417
ID   ABM18575 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054480-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1418
ID   ABR97603 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003059885-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1419
ID   ABR80703 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049740-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1420
ID   ABM01314 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049770-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1421
ID   ABR88816 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003073169-A1.
PD   17-APR-2003.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1422
ID   ABM13568 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064457-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1423
ID   ABM20952 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068711-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1424
ID   ABO42083 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003049745-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1425
ID   ABO42693 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003049751-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1426
ID   ABM10213 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003067478-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1427
ID   ABO38728 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003066773-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
          Query Match          9.9%;  Score 309;  DB 6;  Length 649;
          Best Local Similarity 22.3%;  Pred. No. 5.2e-11;
RESULT 1428
ID   ABM32968 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003071185-A1.
PD   17-APR-2003.
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PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1429
ID   ABM22782 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003087373-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1430
ID   ABM74993 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003096353-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1431
ID   ADA79928 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003073173-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1432
ID   ABR96383 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054458-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1433
ID   ABM02534 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003059886-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1434
ID   ABR86476 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049758-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1435
ID   ABR86781 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049772-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1436
ID   ABM16745 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064448-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1437
ID   ABM29797 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064456-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1438
ID   AB029221 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068693-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1439
ID   ABM24002 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068735-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1440
ID   ABM23392 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068753-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1441
ID   ABM22172 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068742-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1442
ID   AB037813 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068756-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1443
ID   ABM28577 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003082715-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1444
ID   ABM28882 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003082716-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1445
ID   ABM66526 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068737-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1446
ID   ABM75908 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104547-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1447
ID   ABM34188 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003096359-A1.
PD   22-MAY-2003.
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PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1448
ID   ABM34493 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003100061-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1449
ID   ABO20424 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032125-A1.
PD   13-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1450
ID   ABO21339 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003054454-A1.
PD   20-MAR-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1451
ID   ABO22254 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003055222-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1452
ID   ADA20166 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003055222-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1453
ID   ABR96688 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054460-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1454
ID   ABR85866 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049753-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1455
ID   ABR99848 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049763-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1456
ID   ABM00399 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003073172-A1.
PD   17-APR-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1457

ID   ABM00704 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   .US2003073172-A1.
PD   17-APR-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1458
ID   ABO29831 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068700-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1459
ID   ABM23697 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068736-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1460
ID   ABM29492 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068679-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1461
ID   ABO38423 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068767-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1462
ID   ABO45723 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003073182-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1463
ID   ABM20647 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104557-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1464
ID   ADA81655 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003099121-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1465
ID   ABO16761 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003027276-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 5.2e-11;
RESULT 1466
ID   ABO18387 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003044920-A1.

PD 06-MAR-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1467
ID ABO22814 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1468
ID ABO23119 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1469
ID ABR92661 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1470
ID ABR81618 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1471
ID ABM78042 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1472
ID ABR89831 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1473
ID ABM26747 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1474
ID ABM13873 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1475
ID ABO28611 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1476

ID ABO30441 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1477
ID ABM07468 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1478
ID ABM04059 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1479
ID ABO37203 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1480
ID ABO41778 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1481
ID ABO35373 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1482
ID ABM25222 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1483
ID ABO47614 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1484
ID ABO47919 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 5.2e-11;
RESULT 1485
ID ABO48529 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.

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PN   US2003049750-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1486
ID   ABO51579 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003049766-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1487
ID   ABO51884 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003049767-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1488
ID   ABO50664 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003049779-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1489
ID   ABR79788 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040059-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1490
ID   ABM17050 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040078-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1491
ID   ABO18082 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003044918-A1.
PD   06-MAR-2003.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1492
ID   ABO21034 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032132-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1493
ID   ABR96993 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054462-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1494
ID   ABM12348 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064445-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1495
ID   ABM16440 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064449-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1496
ID   ABM24307 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064441-A1.
PD   03-APR-2003.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1497
ID   ABM14788 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068896-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1498
ID   ABM04669 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068712-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1499
ID   ABM06858 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068730-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
RESULT 1500
ID   ABM09298 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003073174-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity  22.3%;  Pred. No. 5.2e-11;
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OM protein - protein search, using sw model

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              GenCore version 6.2
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Run on: January 28, 2007, 17:25:31 ; Search time 52 Seconds
(without alignments)
1006.602 Million cell updates/sec

Title: US-10-677-669-69
Perfect score: 3135
Sequence: 1 MCSRVPLLLPLLLLALGPG.........PLMGFPGPGLQSPLHAKPYI 598

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_AA:*
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7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
2	3135	100.0	598	2	US-09-944-457-69	Sequence 69, Appl
7	3083.5	98.4	673	2	US-09-063-950-2	Sequence 2, Appli
19	337	10.7	653	2	US-09-520-781-10	Sequence 10, Appl
20	337	10.7	653	2	US-09-957-187-10	Sequence 10, Appl
21	337	10.7	653	2	US-09-991-053-10	Sequence 10, Appl
22	333	10.6	590	2	US-09-520-781-12	Sequence 12, Appl
23	333	10.6	590	2	US-09-957-187-12	Sequence 12, Appl
24	333	10.6	590	2	US-09-991-053-12	Sequence 12, Appl
36	322	10.3	605	2	US-09-063-950-5	Sequence 5, Appli
43	320	10.2	660	2	US-09-949-016-6843	Sequence 6843, Ap
48	320	10.2	660	2	US-09-689-486-58	Sequence 58, Appl
55	320	10.2	683	2	US-09-949-016-7267	Sequence 7267, Ap
58	310.5	9.9	674	2	US-09-689-486-59	Sequence 59, Appl
59	310.5	9.9	674	2	US-09-689-486-60	Sequence 60, Appl
60	310.5	9.9	674	2	US-09-973-424A-59	Sequence 59, Appl
61	310.5	9.9	674	2	US-09-973-424A-60	Sequence 60, Appl
62	310	9.9	674	2	US-09-973-424A-75	Sequence 75, Appl
63	310	9.9	662	2	US-09-949-016-10298	Sequence 10298, A
64	308	9.8	649	2	US-09-689-486-57	Sequence 57, Appl
65	308	9.8	649	2	US-09-973-424A-57	Sequence 57, Appl
66	307.5	9.8	674	2	US-09-949-016-7204	Sequence 7204, Ap
67	307.5	9.8	674	2	US-09-689-486-7	Sequence 7, Appli
68	307.5	9.8	674	2	US-09-973-424A-7	Sequence 7, Appli
69	305.5	9.7	664	2	US-09-973-424A-68	Sequence 68, Appl
70	302	9.6	605	1	US-08-190-802A-49	Sequence 49, Appl
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| 71 | 302 | 9.6 | 605 | 2 | US-08-477-346-49 | Sequence 49, Appl |
| 72 | 302 | 9.6 | 605 | 2 | US-08-473-089-49 | Sequence 49, Appl |
| 73 | 302 | 9.6 | 605 | 2 | US-08-487-072A-49 | Sequence 49, Appl |
| 74 | 302 | 9.6 | 605 | 2 | US-09-538-092-1087 | Sequence 1087, Ap |
| 75 | 302 | 9.6 | 623 | 2 | US-09-949-016-10995 | Sequence 10995, A |
| 76 | 301 | 9.6 | 448 | 2 | US-09-520-781-32 | Sequence 32, Appl |
| 77 | 301 | 9.6 | 448 | 2 | US-09-957-187-32 | Sequence 32, Appl |
| 78 | 301 | 9.6 | 448 | 2 | US-09-991-053-32 | Sequence 32, Appl |
| 79 | 298.5 | 9.5 | 649 | 2 | US-09-188-930-305 | Sequence 305, App |
| 80 | 298.5 | 9.5 | 649 | 2 | US-09-312-283C-305 | Sequence 305, App |
| 126 | 284.5 | 9.1 | 745 | 2 | US-10-104-047-2955 | Sequence 2955, Ap |
| 127 | 282.5 | 9.0 | 603 | 2 | US-10-104-047-2960 | Sequence 2960, Ap |
| 128 | 281.5 | 9.0 | 603 | 1 | US-08-190-802A-50 | Sequence 50, Appl |
| 130 | 281.5 | 9.0 | 603 | 2 | US-08-473-089-50 | Sequence 50, Appl |
| 131 | 281.5 | 9.0 | 603 | 2 | US-08-487-072A-50 | Sequence 50, Appl |
| 132 | 271.5 | 8.7 | 353 | 2 | US-08-986-485-6 | Sequence 6, Appli |
| 133 | 271.5 | 8.7 | 1504 | 2 | US-10-037-417-98 | Sequence 98, Appl |
| 134 | 271 | 8.6 | 473 | 2 | US-09-949-016-8448 | Sequence 8448, Ap |
| 142 | 259 | 8.3 | 610 | 1 | US-07-821-717B-6 | Sequence 6, Appli |
| 143 | 259 | 8.3 | 610 | 1 | US-08-119-262B-6 | Sequence 6, Appli |
| 144 | 259 | 8.3 | 610 | 1 | US-08-135-929A-11 | Sequence 11, Appl |
| 145 | 258 | 8.3 | 610 | 1 | US-08-234-265A-11 | Sequence 11, Appl |
| 146 | 258 | 8.2 | 1523 | 2 | US-09-182-024A-2 | Sequence 2, Appli |
| 166 | 255.5 | 8.1 | 1480 | 2 | US-09-191-647-7 | Sequence 7, Appli |
| 167 | 255.5 | 8.1 | 1480 | 2 | US-09-540-245A-7 | Sequence 7, Appli |
| 168 | 255.5 | 8.1 | 1480 | 2 | US-09-540-153-7 | Sequence 7, Appli |
| 169 | 255.5 | 8.1 | 1480 | 2 | US-09-182-024A-5 | Sequence 5, Appli |
| 170 | 255.5 | 8.1 | 1480 | 2 | US-10-289-776-7 | Sequence 7, Appli |
| 171 | 255.5 | 8.1 | 1480 | 5 | PCT-US91-09055-2 | Sequence 2, Appli |
| 172 | 253 | 8.1 | 567 | 2 | US-10-037-417-106 | Sequence 106, App |
| 173 | 252 | 8.1 | 566 | 2 | US-09-775-803-12 | Sequence 12, Appl |
| 174 | 252 | 8.0 | 567 | 2 | US-10-037-417-105 | Sequence 105, App |
| 175 | 251 | 8.0 | 622 | 2 | US-10-188-495-48 | Sequence 48, Appl |
| 176 | 249.5 | 8.0 | 789 | 2 | US-09-831-846-2 | Sequence 2, Appli |
| 177 | 248 | 7.9 | 481 | 2 | US-09-063-753-2 | Sequence 2, Appli |
| 178 | 248 | 7.9 | 485 | 2 | US-09-949-016-8704 | Sequence 8704, Ap |
| 179 | 247.5 | 7.9 | 1525 | 2 | US-09-191-647-2 | Sequence 2, Appli |
| 180 | 247.5 | 7.9 | 1525 | 2 | US-09-540-245A-2 | Sequence 2, Appli |
| 181 | 247.5 | 7.9 | 1525 | 2 | US-09-540-153-2 | Sequence 2, Appli |
| 182 | 247.5 | 7.9 | 1529 | 2 | US-10-289-776-2 | Sequence 2, Appli |
| 183 | 247.5 | 7.9 | 1529 | 2 | US-10-188-495-67 | Sequence 67, Appl |
| 184 | 246.5 | 7.9 | 1529 | 2 | US-09-312-283C-396 | Sequence 396, App |
| 185 | 244 | 7.8 | 708 | 2 | US-09-131-648-2 | Sequence 2, Appli |
| 203 | 243.5 | 7.8 | 312 | 2 | US-10-037-417-108 | Sequence 108, App |
| 204 | 242.5 | 7.7 | 545 | 3 | US-10-114-270-38 | Sequence 38, Appl |
| 205 | 242.5 | 7.7 | 545 | 3 | US-10-114-270-40 | Sequence 40, Appl |
| 206 | 241 | 7.7 | 380 | 2 | US-09-461-325-161 | Sequence 161, App |
| 207 | 241 | 7.7 | 380 | 2 | US-10-012-542-161 | Sequence 161, App |
| 208 | 241 | 7.7 | 380 | 2 | US-10-115-123-161 | Sequence 161, App |
| 209 | 240 | 7.7 | 560 | 2 | US-08-592-500-2 | Sequence 2, Appli |
| 210 | 240 | 7.7 | 560 | 2 | US-08-195-006-2 | Sequence 2, Appli |
| 211 | 240 | 7.7 | 560 | 2 | US-09-063-950-4 | Sequence 4, Appli |
| 212 | 240 | 7.7 | 560 | 2 | US-09-775-803-14 | Sequence 14, Appl |
| 213 | 240 | 7.7 | 560 | 5 | PCT-US94-07644A-2 | Sequence 2, Appli |
| 214 | 236.5 | 7.5 | 231 | 5 | PCT-US91-09055-3 | Sequence 3, Appli |
| 215 | 236.5 | 7.5 | 544 | 2 | US-10-086-485-7 | Sequence 7, Appli |
| 216 | 230.5 | 7.4 | 544 | 2 | US-10-068-426-1 | Sequence 1, Appli |
| 217 | 227 | 7.2 | 568 | 2 | US-09-673-245-14 | Sequence 14, Appl |
| 218 | 226.5 | 7.2 | 544 | 2 | US-10-068-426-3 | Sequence 3, Appli |
| 219 | 226.5 | 7.2 | 557 | 2 | US-10-037-417-95 | Sequence 95, Appl |
| 220 | 226.5 | 7.2 | 719 | 2 | US-10-094-749-2001 | Sequence 2001, Ap |
| 221 | 225 | 7.2 | 544 | 2 | US-10-068-426-2 | Sequence 2, Appli |
| 222 | 225 | 7.2 | 735 | 2 | US-09-191-647-9 | Sequence 9, Appli |
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| 225 | 225 | 7.2 | 735 | 2 | US-10-289-776-9 | Sequence 9, Appli |
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| 670 | 133.5 | 4.2 | 1166 | US-10-101-464A-900 | 2 | Sequence 900, App |
| 671 | 133 | 4.2 | 652 | US-10-104-047-3364 | 2 | Sequence 3364, Ap |
| 672 | 133 | 4.2 | 4391 | US-10-006-011A-2 | 2 | Sequence 2, Appli |
| 673 | 132.5 | 4.2 | 390 | US-08-460-576-2 | 2 | Sequence 2, Appli |
| 674 | 132.5 | 4.2 | 463 | US-08-162-402B-9 | 1 | Sequence 9, Appli |
| 675 | 132.5 | 4.2 | 579 | US-09-325-932A-185 | 2 | Sequence 185, App |
| 676 | 132.5 | 4.2 | 583 | US-09-641-612-2 | 2 | Sequence 2, Appli |
| 677 | 132.5 | 4.2 | 2035 | US-08-046-585-5 | 2 | Sequence 5, Appli |
| 678 | 132.5 | 4.2 | 2035 | US-08-393-703-5 | 1 | Sequence 5, Appli |
| 679 | 132.5 | 4.2 | 2035 | PCT-US93-11721-5 | 5 | Sequence 5, Appli |
| 680 | 132.5 | 4.2 | 2045 | US-09-949-016-10491 | 2 | Sequence 10491, A |
| 681 | 132.5 | 4.2 | 3122 | US-10-237-551-201 | 2 | Sequence 201, App |
| 682 | 132.5 | 4.2 | 287 | US-10-237-551-250 | 2 | Sequence 250, App |
| 683 | 132 | 4.2 | 465 | US-09-889-737-110 | 2 | Sequence 110, App |
| 684 | 132 | 4.2 | 705 | US-08-162-402B-8 | 1 | Sequence 8, Appli |
| 685 | 132 | 4.2 | 979 | US-10-101-464A-894 | 2 | Sequence 894, App |
| 686 | 132 | 4.2 | 979 | US-08-514-213A-2 | 2 | Sequence 2, Appli |
| 687 | 132 | 4.2 | 1003 | US-09-015-399-5 | 2 | Sequence 5, Appli |
| 688 | 132 | 4.2 | 1003 | US-09-949-016-11260 | 2 | Sequence 11260, A |
| 689 | 131.5 | 4.2 | 461 | US-10-037-417-96 | 2 | Sequence 96, Appl |
| 690 | 131.5 | 4.2 | 571 | US-09-252-991A-30533 | 2 | Sequence 30533, A |
| 691 | 131 | 4.2 | 180 | US-08-986-485-8 | 2 | Sequence 8, Appli |
| 692 | 131 | 4.2 | 227 | US-10-101-464A-666 | 2 | Sequence 666, App |
| 693 | 131 | 4.2 | 279 | US-09-270-767-41558 | 2 | Sequence 41558, A |
| 694 | 131 | 4.2 | 407 | US-09-270-767-46649 | 2 | Sequence 46649, A |
| 695 | 131 | 4.2 | 799 | US-09-180-439-6 | 2 | Sequence 6, Appli |
| 696 | 131 | 4.2 | 947 | US-09-228-986-73 | 2 | Sequence 73, Appl |
| 697 | 131 | 4.2 | 947 | US-10-101-464A-73 | 2 | Sequence 73, Appl |
| 698 | 131 | 4.2 | 1062 | US-09-902-540-16313 | 2 | Sequence 16313, A |
| 699 | 131 | 4.2 | 1196 | US-08-881-706-2 | 2 | Sequence 2, Appli |
| 700 | 131 | 4.2 | 1196 | US-09-823-394-2 | 2 | Sequence 2, Appli |
| 701 | 131 | 4.2 | 1938 | US-09-949-016-6609 | 2 | Sequence 6609, Ap |
| 702 | 130.5 | 4.2 | 843 | US-10-101-464A-893 | 2 | Sequence 893, App |
| 703 | 130.5 | 4.1 | 878 | US-09-556-706B-2 | 2 | Sequence 2, Appli |
| 704 | 130.5 | 4.2 | 878 | US-09-724-418A-2 | 2 | Sequence 2, Appli |
| 705 | 130.5 | 4.2 | 3729 | US-08-804-227C-4 | 1 | Sequence 4, Appli |
| 706 | 130 | 4.1 | 619 | US-10-037-417-34 | 2 | Sequence 34, Appl |
| 707 | 130 | 4.1 | 645 | US-10-114-270-80 | 2 | Sequence 80, Appl |
| 708 | 129.5 | 4.1 | 550 | US-09-252-991A-21295 | 2 | Sequence 21295, A |
| 709 | 129.5 | 4.1 | 912 | PCT-US95-03747-2 | 5 | Sequence 2, Appli |
| 710 | 129.5 | 4.1 | 1251 | US-09-270-767-44030 | 2 | Sequence 4030, App |
| 711 | 129 | 4.1 | 363 | US-09-252-991A-23655 | 2 | Sequence 23655, A |
| 712 | 129 | 4.1 | 823 | US-09-252-991A-26129 | 2 | Sequence 26129, A |
| 713 | 129 | 4.1 | 885 | US-10-101-464A-809 | 2 | Sequence 809, App |
| 714 | 129 | 4.1 | 1133 | US-08-644-271-30 | 2 | Sequence 30, Appl |
| 715 | 129 | 4.1 | 1940 | US-10-077-955-34 | 2 | Sequence 34, Appl |
| 716 | 129 | 4.1 | 1940 | US-10-016-283-34 | 2 | Sequence 34, Appl |
| 717 | 129 | 4.1 | 1940 | US-09-230-652-2 | 2 | Sequence 2, Appli |
| 718 | 129 | 4.1 | 2321 | US-09-612-226-2 | 2 | Sequence 2, Appli |
| 719 | 129 | 4.1 | 2321 | US-08-442-063A-39 | 1 | Sequence 39, Appli |
| 720 | 128.5 | 4.1 | 188 | US-08-836-854-15 | 2 | Sequence 15, Appl |
| 721 | 128.5 | 4.1 | 446 | US-10-104-047-3233 | 2 | Sequence 3233, Ap |
| 722 | 128.5 | 4.1 | 508 | US-10-101-464A-953 | 2 | Sequence 953, App |
| 723 | 128.5 | 4.1 | 653 | | | |

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| 724 | 128.5 | 4.1 | 864 | 2 | US-10-101-464A-896 | Sequence 896, App |
| 725 | 128.5 | 4.1 | 865 | 2 | US-09-902-540-10416 | Sequence 10416, A |
| 726 | 128.5 | 4.1 | 1023 | 1 | US-08-170-891A-2 | Sequence 2, Appli |
| 727 | 128.5 | 4.1 | 1023 | 1 | US-08-567-375-2 | Sequence 2, Appli |
| 728 | 128.5 | 4.1 | 1023 | 2 | US-08-587-680A-2 | Sequence 2, Appli |
| 729 | 128 | 4.1 | 475 | 2 | US-09-252-991A-30242 | Sequence 30242, A |
| 730 | 128 | 4.1 | 538 | 1 | US-08-541-759B-2 | Sequence 2, Appli |
| 731 | 128 | 4.1 | 717 | 2 | US-10-101-464A-810 | Sequence 810, App |
| 732 | 127.5 | 4.1 | 1006 | 2 | US-10-415-147-12 | Sequence 12, Appl |
| 733 | 127.5 | 4.1 | 1006 | 3 | US-10-114-270-84 | Sequence 84, Appl |
| 734 | 127.5 | 4.1 | 1522 | 3 | US-10-144-198-31 | Sequence 31, Appl |
| 735 | 127.5 | 4.1 | 1581 | 2 | US-09-949-002-414 | Sequence 414, App |
| 736 | 127.5 | 4.1 | 3969 | 3 | US-08-061-376-5 | Sequence 5, Appli |
| 737 | 127.5 | 4.1 | 260 | 2 | US-09-538-092-1262 | Sequence 1262, Ap |
| 738 | 127 | 4.0 | 615 | 2 | US-09-270-767-32658 | Sequence 32658, A |
| 739 | 127 | 4.0 | 141 | 2 | US-09-252-991A-26695 | Sequence 26695, A |
| 740 | 126.5 | 4.0 | 141 | 2 | US-09-270-767-32244 | Sequence 32244, A |
| 741 | 126.5 | 4.0 | 659 | 3 | US-09-270-767-47461 | Sequence 47461, A |
| 753 | 126.5 | 4.0 | 659 | 3 | US-09-423-753-3 | Sequence 3, Appli |
| 754 | 126.5 | 4.0 | 685 | 2 | US-10-241-476-3 | Sequence 3, Appli |
| 755 | 126.5 | 4.0 | 685 | 2 | US-08-872-855-2 | Sequence 25, Appl |
| 756 | 126.5 | 4.0 | 685 | 3 | US-09-423-753-25 | Sequence 3, Appli |
| 757 | 126.5 | 4.0 | 685 | 3 | US-09-641-612-7 | Sequence 7, Appli |
| 758 | 126.5 | 4.0 | 919 | 3 | US-10-241-476-25 | Sequence 25, Appl |
| 759 | 126 | 4.0 | 999 | 1 | US-10-101-464A-642 | Sequence 642, App |
| 760 | 126 | 4.0 | 143 | 2 | US-08-473-553A-5 | Sequence 5, Appli |
| 761 | 126 | 4.0 | 152 | 3 | US-09-893-737-190 | Sequence 190, App |
| 762 | 126 | 4.0 | 775 | 3 | US-09-270-767-33594 | Sequence 33594, A |
| 763 | 126 | 4.0 | 1485 | 2 | US-09-949-016-8799 | Sequence 8799, Ap |
| 764 | 126 | 4.0 | 1821 | 3 | US-09-762-569-4 | Sequence 4, Appli |
| 765 | 125.5 | 4.0 | 440 | 2 | US-09-949-016-5938 | Sequence 5938, Ap |
| 785 | 125.5 | 4.0 | 440 | 2 | US-08-985-335-3 | Sequence 3, Appli |
| 786 | 125.5 | 4.0 | 764 | 2 | US-09-410-372-3 | Sequence 54, Appl |
| 787 | 125.5 | 4.0 | 764 | 2 | US-07-741-453A-54 | Sequence 60, Appl |
| 788 | 125.5 | 4.0 | 1129 | 2 | US-07-741-453A-60 | Sequence 2, Appli |
| 789 | 125 | 5.0 | 419 | 2 | US-09-023-905A-2 | Sequence 237, App |
| 790 | 125 | 4.0 | 757 | 2 | US-10-002-344A-237 | Sequence 25918, A |
| 791 | 125 | 4.0 | 1139 | 2 | US-09-252-991A-25918 | Sequence 20408, A |
| 792 | 125 | 4.0 | 2023 | 2 | US-09-252-991A-20408 | Sequence 8, Appli |
| 793 | 125 | 4.0 | 2026 | 2 | US-09-491-356C-8 | Sequence 86, Appl |
| 794 | 125 | 4.0 | 2124 | 2 | US-09-487-558B-86 | Sequence 1377, Ap |
| 795 | 125 | 4.0 | 2294 | 3 | US-09-538-092-1377 | Sequence 17231, A |
| 796 | 125 | 4.0 | 107 | 2 | US-09-252-991A-17231 | Sequence 61021, A |
| 797 | 124.5 | 4.0 | 283 | 3 | US-09-270-767-61021 | Sequence 4, Appli |
| 798 | 124.5 | 4.0 | 298 | 2 | US-10-211-689-4 | Sequence 22, Appl |
| 799 | 124.5 | 4.0 | 298 | 2 | US-09-992-095B-22 | Sequence 17, Appl |
| 800 | 124.5 | 4.0 | 298 | 2 | US-09-232-160-17 | Sequence 87, Appl |
| 801 | 124.5 | 4.0 | 298 | 3 | US-09-800-729-87 | Sequence 121, App |
| 802 | 124.5 | 4.0 | 298 | 3 | US-09-800-729-121 | Sequence 22, Appl |
| 803 | 124.5 | 4.0 | 298 | 2 | US-09-949-016-9817 | Sequence 9817, Ap |
| 804 | 124.5 | 4.0 | 307 | 2 | US-09-949-016-9818 | Sequence 9818, Ap |
| 805 | 124.5 | 4.0 | 307 | 3 | US-10-000-489-22 | Sequence 22, Appl |
| 806 | 124.5 | 4.0 | 307 | 2 | US-09-832-129-50 | Sequence 50, Appl |
| 807 | 124.5 | 4.0 | 623 | 2 | US-10-211-689-2 | Sequence 2, Appli |
| 808 | 124.5 | 4.0 | 998 | 2 | US-09-648-281-2 | Sequence 19, Appl |
| 809 | 124.5 | 4.0 | 1042 | 3 | US-09-707-919A-19 | Sequence 19, Appl |
| 827 | 124.5 | 4.0 | 1709 | 2 | US-09-083-268-3 | Sequence 3, Appli |
| 828 | 124 | 4.0 | 277 | 2 | US-08-981-998A-3 | Sequence 58, Appl |
| 829 | 124 | 4.0 | 707 | 2 | US-10-228-986-80 | Sequence 80, Appl |
| 830 | 124 | 4.0 | 707 | 2 | US-10-101-464A-80 | Sequence 80, Appl |
| 831 | 124 | 4.0 | 1457 | 2 | US-08-665-255-27 | Sequence 27, Appl |
| 832 | 124 | 4.0 | 1457 | 2 | US-08-762-500-27 | Sequence 27, Appl |
| 833 | 124 | 4.0 | 1472 | 2 | US-09-032-438C-119 | Sequence 119, App |
| 834 | 124 | 4.0 | 1472 | 2 | US-09-041-886-19 | Sequence 19, Appl |
| 835 | 124 | 4.0 | 1312 | 2 | US-09-648-281-2 | Sequence 2, Appli |
| 836 | 124 | 4.0 | 1312 | 2 | US-09-707-919A-19 | Sequence 19, Appl |
| 837 | 124 | 4.0 | 1312 | 2 | US-09-083-268-3 | Sequence 3, Appli |
| 838 | 123.5 | 3.9 | 1312 | 2 | US-08-981-998A-3 | Sequence 3, Appli |
| 839 | 123.5 | 3.9 | 1312 | 2 | US-10-101-464A-898 | Sequence 898, App |
| 840 | 123.5 | 3.9 | 383 | 3 | US-09-252-991A-23688 | Sequence 23688, A |
| 841 | 123.5 | 3.9 | 383 | 3 | | |
| 842 | 123 | 3.9 | 526 | 2 | | |
| 843 | 123 | 3.9 | 526 | 2 | | |

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| No | Score | Ratio | Len | Ct | Application No | Sequence |
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| 844 | 123 | 3.9 | 557 | 2 | US-09-248-796A-26892 | Sequence 26892, A |
| 845 | 123 | 3.9 | 888 | 1 | US-08-445-640-35 | Sequence 35, Appl |
| 846 | 123 | 3.9 | 888 | 2 | US-08-170-558-35 | Sequence 35, Appl |
| 847 | 123 | 3.9 | 888 | 2 | US-08-447-314-35 | Sequence 35, Appl |
| 848 | 123 | 3.9 | 888 | 2 | US-08-445-461-35 | Sequence 35, Appl |
| 849 | 123 | 3.9 | 888 | 2 | US-09-223-490-35 | Sequence 35, Appl |
| 850 | 123 | 3.9 | 888 | 3 | US-10-646-760-35 | Sequence 35, Appl |
| 851 | 123 | 3.9 | 924 | 2 | US-08-481-130-28 | Sequence 28, Appl |
| 852 | 123 | 3.9 | 924 | 1 | US-08-656-984A-28 | Sequence 28, Appl |
| 853 | 123 | 3.9 | 924 | 1 | US-08-485-604-28 | Sequence 28, Appl |
| 854 | 123 | 3.9 | 924 | 1 | US-08-487-595-28 | Sequence 28, Appl |
| 855 | 122.5 | 3.9 | 335 | 3 | US-10-114-270-34 | Sequence 34, Appl |
| 856 | 122.5 | 3.9 | 335 | 2 | US-10-114-270-36 | Sequence 36, Appl |
| 857 | 122.5 | 3.9 | 494 | 2 | US-09-248-796A-16546 | Sequence 16546, A |
| 858 | 122.5 | 3.9 | 585 | 2 | US-09-641-612-5 | Sequence 5, Appli |
| 859 | 122.5 | 3.9 | 596 | 2 | US-09-252-991A-18875 | Sequence 18875, A |
| 860 | 122.5 | 3.9 | 968 | 2 | US-09-180-439-3 | Sequence 3, Appli |
| 861 | 122.5 | 3.9 | 968 | 2 | US-09-180-439-4 | Sequence 3, Appli |
| 862 | 122.5 | 3.9 | 1016 | 2 | US-09-180-439-8 | Sequence 8, Appli |
| 863 | 122.5 | 3.9 | 1036 | 2 | US-09-771-161A-255 | Sequence 255, App |
| 864 | 122.5 | 3.9 | 1036 | 2 | US-09-771-161A-256 | Sequence 256, App |
| 865 | 122 | 3.9 | 191 | 2 | US-09-461-325-186 | Sequence 186, App |
| 866 | 122 | 3.9 | 191 | 2 | US-10-012-542-186 | Sequence 186, App |
| 867 | 122 | 3.9 | 191 | 2 | US-10-115-123-186 | Sequence 186, App |
| 868 | 122 | 3.9 | 206 | 2 | US-09-461-325-412 | Sequence 412, App |
| 869 | 122 | 3.9 | 206 | 2 | US-10-012-542-412 | Sequence 412, App |
| 870 | 122 | 3.9 | 206 | 2 | US-10-115-123-412 | Sequence 412, App |
| 871 | 122 | 3.9 | 312 | 2 | US-09-270-767-31750 | Sequence 31750, A |
| 872 | 122 | 3.9 | 328 | 2 | US-08-414-926A-9 | Sequence 9, Appli |
| 873 | 122 | 3.9 | 328 | 2 | US-09-926-922-9 | Sequence 9, Appli |
| 874 | 122 | 3.9 | 328 | 2 | US-09-253-682-9 | Sequence 9, Appli |
| 875 | 122 | 3.9 | 328 | 1 | US-09-527-657-9 | Sequence 9, Appli |
| 876 | 122 | 3.9 | 481 | 2 | US-09-892-100-9 | Sequence 9, Appli |
| 877 | 122 | 3.9 | 495 | 2 | US-09-949-016-9748 | Sequence 9748, Ap |
| 878 | 122 | 3.9 | 515 | 2 | US-09-252-991A-31949 | Sequence 31949, A |
| 879 | 122 | 3.9 | 527 | 2 | US-09-252-991A-28127 | Sequence 28127, A |
| 880 | 122 | 3.9 | 527 | 2 | US-09-370-838-216 | Sequence 216, App |
| 881 | 122 | 3.9 | 529 | 2 | US-09-854-133-216 | Sequence 216, App |
| 882 | 121.5 | 3.9 | 320 | 2 | US-09-325-932A-190 | Sequence 190, App |
| 883 | 121.5 | 3.9 | 344 | 2 | US-10-094-749-2951 | Sequence 2951, Ap |
| 884 | 121.5 | 3.9 | 477 | 2 | US-09-252-991A-19831 | Sequence 19831, A |
| 885 | 121.5 | 3.9 | 695 | 2 | US-09-248-796A-18020 | Sequence 18020, A |
| 886 | 121.5 | 3.9 | 818 | 2 | US-10-104-047-2546 | Sequence 2546, Ap |
| 887 | 121.5 | 3.9 | 1225 | 2 | US-09-501-171-4 | Sequence 4, Appli |
| 888 | 121.5 | 3.9 | 1225 | 2 | US-09-949-016-6063 | Sequence 6063, Ap |
| 889 | 121.5 | 3.9 | 1251 | 5 | PCT-US95-02251-3 | Sequence 3, Appli |
| 890 | 121.5 | 3.9 | 1252 | 2 | US-09-199-780-3 | Sequence 3, Appli |
| 891 | 121.5 | 3.9 | 1252 | 2 | US-09-228-986-72 | Sequence 72, Appl |
| 892 | 121.5 | 3.9 | 1253 | 2 | US-08-316-650-3 | Sequence 3, Appli |
| 893 | 121.5 | 3.9 | 1253 | 2 | US-08-479-722B-4 | Sequence 4, Appli |
| 894 | 121 | 3.8 | 499 | 3 | US-09-592-685-4 | Sequence 4, Appli |
| 895 | 121 | 3.8 | 739 | 2 | US-09-049-672A-1 | Sequence 1, Appli |
| 896 | 121 | 3.8 | 910 | 2 | US-09-902-540-10606 | Sequence 10606, A |
| 897 | 121 | 3.8 | 910 | 2 | US-08-442-063A-36 | Sequence 36, Appl |
| 898 | 121 | 3.8 | 910 | 2 | US-10-101-464A-72 | Sequence 72, Appl |
| 899 | 121 | 3.8 | 955 | 2 | US-10-094-749-2652 | Sequence 2652, Ap |
| 900 | 121 | 3.8 | 1139 | 3 | US-09-513-505-4 | Sequence 4, Appli |
| 901 | 120.5 | 3.8 | 1742 | 1 | US-09-958-359-23 | Sequence 23, Appl |
| 902 | 120.5 | 3.8 | 54 | 2 | US-09-973-424A-71 | Sequence 71, Appl |
| 903 | 120.5 | 3.8 | 141 | 2 | US-08-442-063A-36 | Sequence 36, Appl |
| 904 | 120.5 | 3.8 | 426 | 2 | US-09-252-991A-24450 | Sequence 24450, A |
| 905 | 120.5 | 3.8 | 464 | 2 | US-09-716-964B-4 | Sequence 4, Appli |
| 906 | 120.5 | 3.8 | 562 | 4 | US-09-902-540-13269 | Sequence 13269, A |
| 907 | 120.5 | 3.8 | 787 | 2 | US-09-721-383-2 | Sequence 2, Appli |
| 908 | 120.5 | 3.8 | 787 | 2 | US-09-721-137-2 | Sequence 2, Appli |
| 909 | 120.5 | 3.8 | 787 | 2 | US-09-721-251-2 | Sequence 2, Appli |
| 910 | 120.5 | 3.8 | 787 | 2 | US-10-114-764-2 | Sequence 2, Appli |
| 911 | 120.5 | 3.8 | 998 | 2 | US-10-101-464A-931 | Sequence 931, App |
| 912 | 120.5 | 3.8 | 1104 | 2 | US-09-981-953A-4 | Sequence 4, Appli |
| 913 | 120.5 | 3.8 | 1587 | 2 | US-09-949-002-354 | Sequence 354, App |
| 914 | 120.5 | 3.8 | 1610 | 2 | US-09-548-473B-4 | Sequence 4, Appli |
| 915 | 120.5 | 3.8 | 1665 | 2 | US-09-858-664A-2 | Sequence 2, Appli |
| 916 | 120.5 | 3.8 | 1665 | 2 | US-10-274-978-2 | Sequence 2, Appli |

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| Idx | Score | S | Len | N | Application | Sequence |
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| 917 | 120.5 | 3.8 | 1665 | 2 | US-10-697-263-2 | Sequence 2, Appli |
| 918 | 120.5 | 3.8 | 2596 | 2 | US-09-548-473B-6 | Sequence 6, Appli |
| 919 | 120.5 | 3.8 | 2630 | 3 | US-10-077-130-5 | Sequence 5, Appli |
| 920 | 120.5 | 3.8 | 7968 | 3 | US-09-270-767-33086 | Sequence 33086, A |
| 921 | 120 | 3.8 | 130 | 2 | US-09-270-767-48303 | Sequence 48303, A |
| 922 | 120 | 3.8 | 130 | 2 | US-09-046-736-2 | Sequence 2, Appli |
| 923 | 120 | 3.8 | 467 | 2 | US-08-473-553A-3 | Sequence 3, Appli |
| 924 | 120 | 3.8 | 523 | 1 | US-09-514-245-22 | Sequence 22, Appl |
| 925 | 120 | 3.8 | 569 | 2 | US-09-906-779-4 | Sequence 4, Appli |
| 926 | 120 | 3.8 | 603 | 2 | US-09-758-759-125 | Sequence 125, App |
| 927 | 120 | 3.8 | 696 | 2 | US-10-094-749-2315 | Sequence 2315, Ap |
| 928 | 120 | 3.8 | 710 | 2 | US-10-185-432-17 | Sequence 17, Appl |
| 929 | 120 | 3.8 | 2556 | 2 | US-08-899-232-2 | Sequence 2, Appli |
| 930 | 120 | 3.8 | 2556 | 1 | US-09-121-457-2 | Sequence 2, Appli |
| 931 | 120 | 3.8 | 520 | 2 | US-09-107-433-3721 | Sequence 3721, Ap |
| 932 | 119.5 | 3.8 | 608 | 2 | US-09-949-016-11148 | Sequence 11148, A |
| 933 | 119.5 | 3.8 | 608 | 2 | US-09-949-016-11149 | Sequence 11149, A |
| 934 | 119.5 | 3.8 | 608 | 2 | US-09-949-016-11150 | Sequence 11150, A |
| 935 | 119.5 | 3.8 | 608 | 2 | US-09-949-016-11151 | Sequence 11151, A |
| 936 | 119.5 | 3.8 | 1034 | 2 | US-09-252-991A-28921 | Sequence 28921, A |
| 937 | 119.5 | 3.8 | 1048 | 2 | US-09-171-699-10 | Sequence 10, Appl |
| 938 | 119.5 | 3.8 | 1149 | 2 | US-09-560-005-5 | Sequence 5, Appli |
| 939 | 119.5 | 3.8 | 1149 | 2 | US-09-418-540-5 | Sequence 5, Appli |
| 940 | 119.5 | 3.8 | 1149 | 2 | US-09-969-528-5 | Sequence 5, Appli |
| 941 | 119.5 | 3.8 | 1345 | 3 | US-10-433-794-17 | Sequence 17, Appl |
| 942 | 119.5 | 3.8 | 1596 | 2 | US-09-538-092-887 | Sequence 887, App |
| 943 | 119.5 | 3.8 | 304 | 2 | US-10-101-464A-717 | Sequence 717, App |
| 944 | 119 | 3.8 | 319 | 2 | US-08-630-172-12 | Sequence 12, Appl |
| 945 | 119 | 3.8 | 319 | 2 | US-09-375-419-12 | Sequence 12, Appl |
| 946 | 119 | 3.8 | 528 | 2 | US-08-928-213B-8 | Sequence 8, Appli |
| 947 | 119 | 3.8 | 593 | 2 | US-09-252-991A-20441 | Sequence 20441, A |
| 948 | 119 | 3.8 | 784 | 2 | US-09-982-308B-23 | Sequence 23, Appl |
| 949 | 119 | 3.8 | 1081 | 2 | US-09-369-364A-17 | Sequence 17, Appl |
| 950 | 118.5 | 3.8 | 171 | 2 | US-09-270-767-43049 | Sequence 43049, A |
| 951 | 118.5 | 3.8 | 422 | 2 | US-09-949-016-8251 | Sequence 8251, Ap |
| 952 | 118.5 | 3.8 | 430 | 2 | US-09-949-016-8782 | Sequence 8782, Ap |
| 953 | 118.5 | 3.8 | 486 | 1 | US-10-450-360-2 | Sequence 2, Appli |
| 954 | 118.5 | 3.8 | 883 | 2 | US-10-188-495-72 | Sequence 72, Appl |
| 955 | 118 | 3.8 | 1166 | 2 | US-10-104-047-2949 | Sequence 2949, Ap |
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| 959 | 118 | 3.8 | 462 | 2 | US-09-252-991A-20814 | Sequence 20814, A |
| 960 | 118 | 3.8 | 947 | 2 | US-09-252-991A-21335 | Sequence 21335, A |
| 961 | 118 | 3.8 | 1044 | 2 | US-09-252-991A-18853 | Sequence 18853, A |
| 962 | 118 | 3.8 | 1064 | 2 | US-09-252-991A-17508 | Sequence 17508, A |
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| 967 | 117.5 | 3.7 | 2471 | 1 | US-08-083-590A-19 | Sequence 19, Appl |
| 968 | 117.5 | 3.7 | 2471 | 1 | US-08-532-384-19 | Sequence 19, Appl |
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| 970 | 117.5 | 3.7 | 129 | 5 | PCT-US95-09172-4 | Sequence 4, Appli |
| 971 | 117.5 | 3.7 | 189 | 2 | US-10-101-464A-730 | Sequence 730, App |
| 972 | 117.5 | 3.7 | 247 | 2 | US-10-101-464A-517 | Sequence 517, A |
| 973 | 117.5 | 3.7 | 563 | 2 | US-09-252-991A-17549 | Sequence 17549, A |
| 974 | 117.5 | 3.7 | 190 | 1 | US-08-441-629-4 | Sequence 4, Appli |
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| 981 | 117.5 | 3.7 | 635 | 2 | US-08-714-524D-50 | Sequence 50, Appl |
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| 983 | 117.5 | 3.7 | 996 | 2 | US-10-101-464A-933 | Sequence 933, App |
| 984 | 117.5 | 3.7 | 1118 | 2 | US-09-252-991A-24340 | Sequence 24340, A |
| 985 | 117.5 | 3.7 | 1506 | 2 | US-10-142-650-4 | Sequence 4, Appli |
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| 993 | 117.5 | 3.7 | 1706 | 2 | US-09-528-706-2 | Sequence 2, Appli |
| 994 | 117.5 | 3.7 | 1706 | 2 | US-10-142-650-2 | Sequence 2, Appli |
| 995 | 117.5 | 3.7 | 1706 | 2 | US-10-142-650-3 | Sequence 3, Appli |
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| 1008 | 117 | 3.7 | 1193 | 2 | US-08-611-729A-10 | Sequence 10, Appl |
| 1009 | 117 | 3.7 | 1193 | 2 | US-09-195-524-10 | Sequence 8, Appli |
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| 1014 | 117 | 3.7 | 1238 | 2 | US-09-855-722-5 | Sequence 5, Appli |
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| 1017 | 117 | 3.7 | 1257 | 2 | US-09-310-685-6 | Sequence 6, Appli |
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| 1020 | 116.5 | 3.7 | 296 | 2 | US-09-270-767-37980 | Sequence 37980, A |
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| 1050 | 115.5 | 3.7 | 1093 | 5 | PCT-US94-04496-55 | Sequence 55, Appl |
| 1051 | 115 | 3.7 | 305 | 1 | US-09-325-932A-188 | Sequence 188, App |
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| 1062 | 115 | 3.7 | 1219 | 2 | US-10-024-368-4 | Sequence 4, Appli |

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| 1134 | 3.6 | 113 | 1247 | 2 | US-09-501-171-6 | Sequence 6, Appli |
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| 1154 | 3.6 | 112 | 241 | 2 | US-08-411-295F-94 | Sequence 94, Appl |
| 1155 | 3.6 | 112 | 297 | 1 | US-08-580-545B-6 | Sequence 6, Appli |
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| 1175 | 3.6 | 112 | 764 | 2 | US-09-826-509-407 | Sequence 407, App |
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| 1177 | 3.6 | 112 | 764 | 2 | US-09-826-509-415 | Sequence 415, App |
| 1178 | 3.6 | 112 | 764 | 2 | US-09-826-509-419 | Sequence 419, App |
| 1179 | 3.6 | 112 | 764 | 2 | US-09-826-509-423 | Sequence 423, App |
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| 1194 | 3.6 | 111.5 | 816 | 2 | US-09-902-540-10602 | Sequence 10602, A |
| 1195 | 3.6 | 111.5 | 1021 | 2 | US-09-266-225D-12 | Sequence 12, Appl |
| 1196 | 3.6 | 111.5 | 841 | 2 | US-09-949-016-9797 | Sequence 9797, Ap |
| 1197 | 3.6 | 111.5 | 1021 | 2 | US-10-101-464A-954 | Sequence 954, App |
| 1198 | 3.6 | 111.5 | 1298 | 1 | US-08-690-473-2 | Sequence 2, Appli |
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| 1200 | 3.6 | 111.5 | 1298 | 2 | US-08-843-659-2 | Sequence 2, Appli |
| 1201 | 3.5 | 111.5 | 239 | 2 | US-09-825-288A-2 | Sequence 2, Appli |
| 1202 | 3.5 | 111 | 267 | 2 | US-09-252-991A-21250 | Sequence 21250, A |
| 1203 | 3.5 | 111 | 267 | 2 | US-08-818-112-142 | Sequence 142, App |
| 1204 | 3.5 | 111 | 267 | 2 | US-08-818-111-137 | Sequence 137, App |
| 1205 | 3.5 | 111 | 267 | 2 | US-09-056-556-142 | Sequence 142, App |
| 1206 | 3.5 | 111 | 267 | 2 | US-09-072-596-137 | Sequence 137, App |
| 1207 | 3.5 | 111 | 267 | 2 | US-09-072-967-142 | Sequence 142, App |
| 1208 | 3.5 | 111 | 267 | 2 | US-10-193-002-137 | Sequence 137, App |

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| 1210 | 111 | 3.5 | 322 | 2 | US-09-252-991A-29259 | Sequence 29259, A |
| 1211 | 111 | 3.5 | 333 | 2 | US-09-252-991A-19956 | Sequence 19956, A |
| 1212 | 111 | 3.5 | 452 | 2 | US-09-949-016-7289 | Sequence 7289, Ap |
| 1213 | 111 | 3.5 | 454 | 2 | US-08-716-964B-5 | Sequence 5, Appli |
| 1214 | 111 | 3.5 | 492 | 1 | US-08-644-271-32 | Sequence 32, Appl |
| 1215 | 111 | 3.5 | 492 | 2 | US-09-077-955-36 | Sequence 36, Appl |
| 1216 | 111 | 3.5 | 492 | 2 | US-10-016-283-36 | Sequence 36, Appl |
| 1217 | 111 | 3.5 | 595 | 2 | US-09-949-016-7205 | Sequence 7205, Ap |
| 1218 | 111 | 3.5 | 699 | 2 | US-07-757-342D-2 | Sequence 2, Appli |
| 1219 | 111 | 3.5 | 699 | 2 | US-09-461-657B-2 | Sequence 2, Appli |
| 1220 | 111 | 3.5 | 1050 | 2 | US-09-428-711A-16 | Sequence 16, Appl |
| 1221 | 111 | 3.5 | 1109 | 2 | US-09-949-016-10771 | Sequence 10771, A |
| 1222 | 111 | 3.5 | 1203 | 2 | US-09-949-016-6615 | Sequence 6615, Ap |
| 1223 | 111 | 3.5 | 1203 | 2 | US-10-067-457-3 | Sequence 3, Appli |
| 1224 | 111 | 3.5 | 1318 | 1 | US-10-237-551-197 | Sequence 197, App |
| 1225 | 111 | 3.5 | 1358 | 1 | US-08-404-665-4 | Sequence 4, Appli |
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| 1228 | 111 | 3.5 | 1518 | 2 | US-10-142-650-2 | Sequence 2, Appli |
| 1229 | 111 | 3.5 | 1540 | 2 | US-09-949-016-11382 | Sequence 11382, A |
| 1230 | 111 | 3.5 | 1540 | 2 | US-09-949-016-11383 | Sequence 11383, A |
| 1231 | 111 | 3.5 | 1650 | 2 | US-09-252-991A-21798 | Sequence 21798, A |
| 1232 | 111 | 3.5 | 1719 | 1 | US-08-459-568-4 | Sequence 4, Appli |
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| 1234 | 111 | 3.5 | 1719 | 2 | US-08-516-859A-4 | Sequence 4, Appli |
| 1235 | 111 | 3.5 | 1719 | 2 | US-09-586-472-4 | Sequence 4, Appli |
| 1236 | 111 | 3.5 | 1719 | 2 | US-09-528-706-4 | Sequence 4, Appli |
| 1237 | 111 | 3.5 | 1719 | 2 | US-10-024-450-4 | Sequence 4, Appli |
| 1238 | 111 | 3.5 | 1719 | 2 | US-10-142-650-1 | Sequence 1, Appli |
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| 1242 | 111 | 3.5 | 2523 | 1 | US-08-185-432-18 | Sequence 18, Appl |
| 1243 | 111 | 3.5 | 2523 | 2 | US-08-899-232-3 | Sequence 3, Appli |
| 1244 | 111 | 3.5 | 2523 | 2 | US-09-121-157-3 | Sequence 3, Appli |
| 1245 | 110.5 | 3.5 | 273 | 2 | US-09-252-991A-30433 | Sequence 30433, A |
| 1246 | 110.5 | 3.5 | 298 | 2 | US-09-248-796A-26762 | Sequence 26762, A |
| 1247 | 110.5 | 3.5 | 565 | 2 | US-08-937-067-8 | Sequence 8, Appli |
| 1248 | 110.5 | 3.5 | 645 | 2 | US-09-964-899-17 | Sequence 17, Appl |
| 1249 | 110.5 | 3.5 | 675 | 2 | US-09-332-063-2 | Sequence 2, Appli |
| 1250 | 110.5 | 3.5 | 675 | 2 | US-09-332-063-3 | Sequence 3, Appli |
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| 1254 | 110.5 | 3.5 | 1207 | 2 | US-10-098-600B-16 | Sequence 16, Appl |
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| 1257 | 110.5 | 3.5 | 1346 | 2 | US-09-105-537-37 | Sequence 37, Appl |
| 1258 | 110.5 | 3.5 | 1346 | 2 | US-09-141-908-5 | Sequence 5, Appli |
| 1259 | 110.5 | 3.5 | 1346 | 2 | US-09-657-440-4 | Sequence 4, Appli |
| 1260 | 110.5 | 3.5 | 1384 | 2 | US-09-793-708-4 | Sequence 4, Appli |
| 1261 | 110.5 | 3.5 | 1384 | 2 | US-08-976-255-11 | Sequence 11, Appl |
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| 1266 | 110.5 | 3.5 | 11877 | 2 | US-09-105-537-6 | Sequence 6, Appli |
| 1267 | 110 | 3.5 | 195 | 2 | US-09-858-664A-11 | Sequence 11, Appl |
| 1268 | 110 | 3.5 | 195 | 2 | US-10-274-978-12 | Sequence 12, Appl |
| 1269 | 110 | 3.5 | 195 | 2 | US-10-697-263-12 | Sequence 12, Appl |
| 1270 | 110 | 3.5 | 450 | 2 | US-09-369-364A-19 | Sequence 19, Appl |
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| 1272 | 110 | 3.5 | 626 | 2 | US-09-862-027-43 | Sequence 43, Appl |
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| 1275 | 110 | 3.5 | 739 | 2 | US-09-001-951-24 | Sequence 24, Appl |
| 1276 | 110 | 3.5 | 739 | 2 | US-08-818-829-24 | Sequence 24, Appl |
| 1277 | 110 | 3.5 | 746 | 2 | US-09-548-797B-4 | Sequence 4, Appli |
| 1278 | 110 | 3.5 | 2703 | 1 | US-08-185-432-19 | Sequence 19, Appl |
| 1279 | 110 | 3.5 | 2703 | 2 | US-08-899-232-4 | Sequence 4, Appli |
| 1280 | 110 | 3.5 | 2703 | 2 | US-09-121-157-4 | Sequence 4, Appli |
| 1281 | 109.5 | 3.5 | 297 | 2 | US-09-252-991A-32590 | Sequence 32590, A |

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| Sequence 660, App | US-10-101-464A-660 | 381 | 1283 | 2 | 3.5 | 109.5 |
| Sequence 939, App | US-10-101-464A-939 | 400 | 1284 | 2 | 3.5 | 109.5 |
| Patent No. 252556 | 252556-1 | 401 | 1285 | 7 | 3.5 | 109.5 |
| Sequence 246, App | US-08-470-335-246 | 456 | 1286 | 2 | 3.5 | 109.5 |
| Sequence 303, App | US-08-467-602-303 | 456 | 1287 | 2 | 3.5 | 109.5 |
| Sequence 229, App | US-08-411-295F-229 | 456 | 1288 | 2 | 3.5 | 109.5 |
| Sequence 345, App | US-08-467-602-345 | 490 | 1289 | 2 | 3.5 | 109.5 |
| Sequence 271, App | US-08-411-295F-271 | 490 | 1290 | 1 | 3.5 | 109.5 |
| Sequence 8, Appli | US-08-359-705B-8 | 612 | 1291 | 2 | 3.5 | 109.5 |
| Sequence 8, Appli | US-08-286-846A-8 | 612 | 1292 | 2 | 3.5 | 109.5 |
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| Sequence 8, Appli | US-09-156-923-8 | 612 | 1296 | 2 | 3.5 | 109.5 |
| Sequence 25544, A | US-09-252-991A-25544 | 632 | 1297 | 2 | 3.5 | 109.5 |
| Sequence 69, Appl | US-09-228-986-69 | 690 | 1298 | 2 | 3.5 | 109.5 |
| Sequence 69, Appl | US-10-101-464A-69 | 690 | 1299 | 2 | 3.5 | 109.5 |
| Sequence 7806, Ap | US-09-949-016-7806 | 693 | 1300 | 2 | 3.5 | 109.5 |
| Sequence 940, App | US-10-101-464A-940 | 697 | 1301 | 2 | 3.5 | 109.5 |
| Sequence 12, Appl | US-10-004-838-12 | 784 | 1302 | 2 | 3.5 | 109.5 |
| Sequence 8, Appli | US-09-150-460B-8 | 798 | 1303 | 1 | 3.5 | 109.5 |
| Sequence 6, Appli | US-08-359-705B-6 | 839 | 1304 | 2 | 3.5 | 109.5 |
| Sequence 6, Appli | US-08-286-846A-6 | 839 | 1305 | 1 | 3.5 | 109.5 |
| Sequence 6, Appli | US-08-457-880A-6 | 839 | 1306 | 2 | 3.5 | 109.5 |
| Sequence 6, Appli | US-08-444-622A-6 | 839 | 1307 | 2 | 3.5 | 109.5 |
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| Sequence 6, Appli | US-09-156-923-6 | 839 | 1309 | 2 | 3.5 | 109.5 |
| Sequence 25286, A | US-09-252-991A-25286 | 904 | 1310 | 2 | 3.5 | 109 |
| Sequence 8455, Ap | US-09-949-016-8455 | 1235 | 1311 | 2 | 3.5 | 109 |
| Sequence 8456, Ap | US-09-949-016-8456 | 1235 | 1312 | 2 | 3.5 | 109 |
| Sequence 28374, A | US-09-252-991A-28374 | 163 | 1313 | 2 | 3.5 | 109 |
| Sequence 29, Appl | US-08-480-229C-29 | 221 | 1314 | 1 | 3.5 | 109 |
| Sequence 29, Appl | US-08-659-235C-29 | 221 | 1315 | 2 | 3.5 | 109 |
| Sequence 2303, Ap | US-10-094-749-2303 | 259 | 1316 | 2 | 3.5 | 109 |
| Sequence 12, Appl | US-08-978-289-12 | 416 | 1317 | 2 | 3.5 | 109 |
| Sequence 1, Appli | US-09-601-478-1 | 416 | 1318 | 2 | 3.5 | 109 |
| Sequence 4, Appli | US-09-601-478-4 | 416 | 1319 | 2 | 3.5 | 109 |
| Sequence 29241, A | US-09-252-991A-29241 | 433 | 1320 | 2 | 3.5 | 109 |
| Sequence 2, Appli | US-08-136-119-2 | 437 | 1321 | 1 | 3.5 | 109 |
| Sequence 7, Appli | US-08-481-814A-7 | 437 | 1322 | 2 | 3.5 | 109 |
| Sequence 32620, A | US-09-252-991A-32620 | 447 | 1323 | 2 | 3.5 | 109 |
| Sequence 540, App | US-09-949-002-540 | 480 | 1324 | 2 | 3.5 | 109 |
| Sequence 10, Appl | US-08-480-229C-10 | 480 | 1325 | 1 | 3.5 | 109 |
| Sequence 10, Appl | US-08-559-235C-10 | 507 | 1326 | 2 | 3.5 | 109 |
| Sequence 24, Appl | US-09-599-287A-24 | 507 | 1327 | 2 | 3.5 | 109 |
| Sequence 24, Appl | US-10-078-547-24 | 510 | 1328 | 2 | 3.5 | 109 |
| Sequence 25076, A | US-09-252-991A-25076 | 552 | 1329 | 2 | 3.5 | 109 |
| Sequence 23036, A | US-08-252-991A-23036 | 560 | 1330 | 2 | 3.5 | 109 |
| Sequence 25999, A | US-09-252-991A-25999 | 730 | 1331 | 2 | 3.5 | 109 |
| Sequence 2401, Ap | US-10-094-749-2401 | 749 | 1332 | 2 | 3.5 | 109 |
| Sequence 27, Appl | US-09-828-313-27 | 762 | 1333 | 2 | 3.5 | 109 |
| Sequence 114, App | US-08-642-255-114 | 762 | 1334 | 2 | 3.5 | 109 |
| Sequence 26, Appl | US-08-397-633A-26 | 764 | 1335 | 2 | 3.5 | 109 |
| Sequence 53, Appl | US-09-186-350A-53 | 828 | 1336 | 2 | 3.5 | 109 |
| Sequence 934, App | US-10-101-464A-934 | 833 | 1337 | 2 | 3.5 | 109 |
| Sequence 6, Appli | US-08-264-534-6 | 833 | 1338 | 1 | 3.5 | 109 |
| Sequence 2, Appli | US-08-083-590A-2 | 833 | 1339 | 1 | 3.5 | 109 |
| Sequence 6, Appli | US-08-465-500-6 | 833 | 1340 | 1 | 3.5 | 109 |
| Sequence 6, Appli | US-08-346-126-6 | 833 | 1341 | 1 | 3.5 | 109 |
| Sequence 6, Appli | US-08-346-128-6 | 850 | 1342 | 2 | 3.5 | 109 |
| Sequence 2, Appli | US-08-532-384-2 | 850 | 1343 | 1 | 3.5 | 109 |
| Sequence 6, Appli | US-08-893-828-6 | 850 | 1344 | 2 | 3.5 | 109 |
| Sequence 7, Appli | US-08-286-305A-7 | 860 | 1345 | 2 | 3.5 | 109 |
| Sequence 7, Appli | US-08-441-104A-7 | 883 | 1346 | 1 | 3.5 | 109 |
| Sequence 7, Appli | US-08-440-816A-7 | 1145 | 1347 | 2 | 3.5 | 109 |
| Sequence 7, Appli | US-09-417-381A-7 | 1336 | 1348 | 2 | 3.5 | 109 |
| Sequence 28607, A | US-09-252-991A-28607 | 1336 | 1349 | 2 | 3.5 | 109 |
| Sequence 3, Appli | US-10-195-970-3 | | 1350 | 2 | 3.5 | 109 |
| Sequence 6, Appli | US-10-195-970-6 | | 1351 | 2 | 3.5 | 109 |
| Sequence 167, App | US-09-758-759-167 | | 1352 | 2 | 3.5 | 109 |
| Sequence 58, Appl | US-08-231-193A-58 | | 1353 | 1 | 3.5 | 109 |
| Sequence 58, Appl | US-08-486-273A-58 | | 1354 | 1 | 3.5 | 109 |

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| 1358 | 109 | 3.5 | 1336 | 2 | US-09-648-797-58 | Sequence 58, Appl |
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| 1362 | 109 | 3.5 | 1336 | 2 | US-09-945-901-58 | Sequence 58, Appl |
| 1363 | 109 | 3.5 | 1358 | 2 | US-09-949-002-353 | Sequence 353, App |
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| 1377 | 108.5 | 3.5 | 723 | 2 | US-09-068-740A-9 | Sequence 9, Appl |
| 1378 | 108.5 | 3.5 | 723 | 3 | US-09-423-753-27 | Sequence 27, Appl |
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| 1382 | 108.5 | 3.5 | 904 | 2 | US-09-252-991A-23202 | Sequence 23202, A |
| 1383 | 108.5 | 3.5 | 955 | 2 | US-09-252-991A-24254 | Sequence 24254, A |
| 1384 | 108.5 | 3.5 | 1125 | 2 | US-09-513-783A-152 | Sequence 152, App |
| 1385 | 108.5 | 3.5 | 1125 | 2 | US-09-430-656-152 | Sequence 152, App |
| 1386 | 108.5 | 3.5 | 1125 | 2 | US-10-100-957A-152 | Sequence 152, App |
| 1387 | 108.5 | 3.5 | 1184 | 2 | US-09-266-225D-18 | Sequence 18, Appl |
| 1388 | 108.5 | 3.5 | 1519 | 2 | US-09-695-795A-4 | Sequence 4, Appli |
| 1389 | 108.5 | 3.5 | 1527 | 2 | US-09-513-783A-22 | Sequence 22, Appl |
| 1390 | 108.5 | 3.5 | 1610 | 2 | US-09-252-991A-23373 | Sequence 22, Appl |
| 1391 | 108.5 | 3.5 | 1610 | 2 | US-09-430-656-22 | Sequence 22, Appl |
| 1392 | 108.5 | 3.5 | 1610 | 2 | US-10-100-957A-22 | Sequence 22, Appl |
| 1393 | 108 | 3.4 | 51 | 2 | US-09-367-206-5 | Sequence 5, Appli |
| 1394 | 108 | 3.4 | 51 | 2 | US-10-037-417-100 | Sequence 100, App |
| 1395 | 108 | 3.4 | 152 | 2 | US-09-214-909-22 | Sequence 22, Appl |
| 1396 | 108 | 3.4 | 180 | 2 | US-09-133-341-12 | Sequence 12, Appl |
| 1397 | 108 | 3.4 | 180 | 2 | US-09-739-852-12 | Sequence 12, Appl |
| 1398 | 108 | 3.4 | 419 | 2 | US-10-237-551-198 | Sequence 198, App |
| 1399 | 108 | 3.4 | 590 | 2 | US-08-785-310A-5 | Sequence 5, Appli |
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| 1410 | 108 | 3.4 | 1320 | 2 | US-08-462-467B-4 | Sequence 4, Appli |
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| 1414 | 108 | 3.4 | 1711 | 2 | US-09-141-908-2 | Sequence 2, Appli |
| 1415 | 108 | 3.4 | 2887 | 2 | US-09-657-440-1 | Sequence 1, Appli |
| 1416 | 107.5 | 3.4 | 4551 | 2 | US-09-793-708-1 | Sequence 1, Appli |
| 1417 | 107.5 | 3.4 | 4551 | 2 | US-09-105-537-31 | Sequence 31, Appl |
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| 1421 | 107.5 | 3.4 | 134 | 2 | US-10-289-776-12 | Sequence 12, Appl |
| 1422 | 107.5 | 3.4 | 134 | 2 | US-09-270-767-46622 | Sequence 46622, A |
| 1423 | 107.5 | 3.4 | 134 | 2 | US-09-252-991A-22096 | Sequence 22096, A |
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| 1430 | 107.5 | 3.4 | 459 | 2 | US-08-470-335-239 | Sequence 239, App |
| 1431 | 107.5 | 3.4 | 459 | 2 | US-08-467-602-299 | Sequence 299, App |
| 1432 | 107.5 | 3.4 | 459 | 2 | US-08-411-295F-225 | Sequence 225, App |
| 1433 | 107.5 | 3.4 | 493 | 2 | US-08-467-602-341 | Sequence 341, App |
| 1434 | 107.5 | 3.4 | 493 | 2 | US-08-411-295F-267 | Sequence 267, App |
| 1435 | 107.5 | 3.4 | 506 | 2 | US-09-949-016-11282 | Sequence 11282, A |
| 1436 | 107.5 | 3.4 | 520 | 2 | US-09-068-740A-3 | Sequence 3, Appli |
| 1437 | 107.5 | 3.4 | 568 | 2 | US-09-252-991A-19968 | Sequence 19968, A |
| 1438 | 107.5 | 3.4 | 655 | 1 | US-07-736-178C-2 | Sequence 2, Appli |
| 1439 | 107.5 | 3.4 | 660 | 2 | US-10-101-464A-808 | Sequence 808, App |
| 1440 | 107.5 | 3.4 | 691 | 2 | US-09-252-991A-31413 | Sequence 31413, A |
| 1441 | 107.5 | 3.4 | 691 | 2 | US-09-758-759-159 | Sequence 159, App |
| 1442 | 107.5 | 3.4 | 723 | 2 | US-09-641-612-6 | Sequence 6, Appli |
| 1443 | 107.5 | 3.4 | 787 | 2 | US-09-252-991A-19991 | Sequence 19991, A- |
| 1444 | 107.5 | 3.4 | 832 | 2 | US-08-981-392-6 | Sequence 6, Appli |
| 1445 | 107.5 | 3.4 | 832 | 2 | US-09-908-322-6 | Sequence 6, Appli |
| 1446 | 107.5 | 3.4 | 984 | 1 | US-08-673-789-9 | Sequence 9, Appli |
| 1447 | 107.5 | 3.4 | 998 | 2 | US-09-949-016-6695 | Sequence 6695, Ap |
| 1448 | 107.5 | 3.4 | 1001 | 2 | US-10-415-147-3 | Sequence 3, Appli |
| 1449 | 107.5 | 3.4 | 1088 | 2 | US-09-233-857-13 | Sequence 13, Appl |
| 1450 | 107.5 | 3.4 | 1135 | 1 | US-08-574-959A-7 | Sequence 7, Appli |
| 1451 | 107.5 | 3.4 | 1135 | 2 | US-09-157-014-7 | Sequence 7, Appli |
| 1452 | 107.5 | 3.4 | 1327 | 1 | US-09-949-016-8412 | Sequence 8412, Ap |
| 1453 | 107 | 3.4 | 131 | 1 | US-08-650-598-3 | Sequence 3, Appli |
| 1454 | 107 | 3.4 | 232 | 2 | US-09-149-476-623 | Sequence 623, App |
| 1455 | 107 | 3.4 | 288 | 2 | US-09-252-991A-27676 | Sequence 27676, A |
| 1456 | 107 | 3.4 | 354 | 2 | US-09-949-016-6051 | Sequence 6051, Ap |
| 1457 | 107 | 3.4 | 358 | 2 | US-09-949-016-8148 | Sequence 8148, Ap |
| 1458 | 107 | 3.4 | 360 | 2 | US-09-248-796A-18991 | Sequence 18991, A |
| 1459 | 107 | 3.4 | 369 | 2 | US-09-252-991A-29670 | Sequence 29670, A |
| 1460 | 107 | 3.4 | 492 | 2 | US-09-252-991A-23619 | Sequence 23619, A |
| 1461 | 107 | 3.4 | 500 | 3 | US-09-423-753-2 | Sequence 2, Appli |
| 1462 | 107 | 3.4 | 500 | 2 | US-09-241-476-2 | Sequence 2, Appli |
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| 1464 | 107 | 3.4 | 593 | 2 | US-08-981-392-68 | Sequence 68, Appl |
| 1465 | 107 | 3.4 | 615 | 2 | US-09-908-322-68 | Sequence 68, Appl |
| 1466 | 107 | 3.4 | 759 | 2 | US-09-964-899-15 | Sequence 15, Appl |
| 1467 | 107 | 3.4 | 793 | 2 | US-09-949-002-301 | Sequence 301, App |
| 1468 | 107 | 3.4 | 806 | 2 | US-09-252-991A-19071 | Sequence 19071, A |
| 1469 | 107 | 3.4 | 1241 | 2 | US-09-252-991A-29395 | Sequence 29395, A |
| 1470 | 107 | 3.4 | 1315 | 2 | US-09-588-256-10 | Sequence 10, Appl |
| 1471 | 106.5 | 3.4 | 157 | 2 | US-08-945-983-2 | Sequence 2, Appli |
| 1472 | 106.5 | 3.4 | 157 | 2 | US-08-714-741-34 | Sequence 34, Appl |
| 1473 | 106.5 | 3.4 | 157 | 2 | US-08-899-595-3 | Sequence 3, Appli |
| 1474 | 106.5 | 3.4 | 176 | 2 | US-08-981-392-68 | Sequence 68, Appl |
| 1475 | 106.5 | 3.4 | 176 | 2 | US-09-908-322-68 | Sequence 68, Appl |
| 1476 | 106.5 | 3.4 | 247 | 2 | US-09-310-685-20 | Sequence 20, Appl |
| 1477 | 106.5 | 3.4 | 401 | 2 | US-09-270-767-32581 | Sequence 32581, A |
| 1478 | 106.5 | 3.4 | 420 | 2 | US-09-270-767-47798 | Sequence 47798, A |
| 1479 | 106.5 | 3.4 | 423 | 2 | US-09-252-991A-23672 | Sequence 23672, A |
| 1480 | 106.5 | 3.4 | 423 | 2 | US-09-248-796A-26759 | Sequence 26759, A |
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| 1482 | 106.5 | 3.4 | 464 | 2 | US-08-702-665A-5 | Sequence 5, Appli |
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| 1484 | 106.5 | 3.4 | 464 | 2 | US-09-366-009-7 | Sequence 7, Appli |
| 1485 | 106.5 | 3.4 | 489 | 2 | US-08-809-156B-7 | Sequence 7, Appli |
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| 1487 | 106.5 | 3.4 | 489 | 2 | US-09-366-009-8 | Sequence 8, Appli |
| 1488 | 106.5 | 3.4 | 575 | 2 | US-08-809-156B-8 | Sequence 8, Appli |
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| 1490 | 106.5 | 3.4 | 642 | 2 | US-08-909-983-4 | Sequence 4, Appli |
| 1491 | 106.5 | 3.4 | 974 | 1 | PCT-US94-07297-41 | Sequence 41, Appl |
| 1492 | 106.5 | 3.4 | 1003 | 2 | US-09-041-886-23 | Sequence 23, Appl |
| 1493 | 106.5 | 3.4 | 1003 | 2 | US-09-538-092-1209 | Sequence 1209, Appl |
| 1494 | 106.5 | 3.4 | 1003 | 1 | US-09-252-991A-29427 | Sequence 29427, A |
| 1495 | 106.5 | 3.4 | 1075 | 5 | US-09-914-259-37 | Sequence 37, Appl |
| 1496 | 106.5 | 3.4 | 1185 | 2 | US-09-538-092-1081 | Sequence 1081, Ap |
| 1497 | 106.5 | 3.4 | 1185 | 2 | | |
| 1498 | 106.5 | 3.4 | 1476 | 2 | | |
| 1499 | 106.5 | 3.4 | 1507 | 2 | | |
| 1500 | 106.5 | 3.4 | 2090 | 2 | | |

ALIGNMENTS

RESULT 1
; Sequence 69, Application US/09866028
Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien

Query Match         100.0%;    Score 3135;   DB 2;   Length 598;
Best Local Similarity   100.0%;    Pred. No. 7.3e-217;
Matches  598;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Db  121  ALRLAGLGLQOLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL  180

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Db  241  SHVTLASPEETRCHFPPKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL  300

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Db  481  PPAVHSNHAPVTQARRGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV  540

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RESULT 2
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; Sequence 69, Application US/09944457
Patent No. 6734288
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069935
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999

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RESULT 3
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; Patent No. 6908993
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,584
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
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; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 12, 1997
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; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
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; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 16, 1997
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945

; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-69

Query Match   100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity   100.0%; Pred. No. 7.3e-217;
Matches   598; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db  121  ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL  180

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Db  181  RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE  240

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Db  241  SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTYATVPTTRPVVREPTALSSSL  300

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Qy   301 APTWLSPTAPATEAPSPSTAPPTVGPVPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
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Qy   541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPFPGPGLQSPLHAKPYI 598
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Db   541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPFPGPGLQSPLHAKPYI 598
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RESULT 4
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; Sequence 69, Application US/09944944
; Patent No. 6929947
; GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin
;   APPLICANT: Botstein,David
;   APPLICANT: Eaton,Dan
;   APPLICANT: Ferrara,Napoleone
;   APPLICANT: Filvaroff,Ellen
;   APPLICANT: Gerritsen,Mary
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul
;   APPLICANT: Grimaldi,Christopher
;   APPLICANT: Gurney,Austin
;   APPLICANT: Hillan,Kenneth
;   APPLICANT: Kljavin,Ivar
;   APPLICANT: Napier,Mary
;   APPLICANT: Roy,Margaret
;   APPLICANT: Tumas,Daniel
;   APPLICANT: Wood,William
;   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION: ACIDS ENCODING THE SAME
;   FILE REFERENCE: P2548P1C1
;   CURRENT APPLICATION NUMBER: US/09/944,944
;   CURRENT FILING DATE: 2001-09-26
;   PRIOR APPLICATION NUMBER: 09/866,028
;   PRIOR FILING DATE: 2001-05-25
;   PRIOR APPLICATION NUMBER: 60/067,411
;   PRIOR FILING DATE: December 11, 1997
;   PRIOR APPLICATION NUMBER: 60/069,278
;   PRIOR FILING DATE: December 3, 1997
;   PRIOR APPLICATION NUMBER: 60/069,334
;   PRIOR FILING DATE: December 11, 1997
;   PRIOR APPLICATION NUMBER: 60/069,702
;   PRIOR FILING DATE: December 11, 1997
;   PRIOR APPLICATION NUMBER: 60/069335
;   PRIOR APPLICATION NUMBER: 60/069,425
;   PRIOR FILING DATE: December 11, 1997
;   PRIOR APPLICATION NUMBER: 60/069,696
;   PRIOR FILING DATE: December 12, 1997
;   PRIOR APPLICATION NUMBER: 60/069,694
;   PRIOR FILING DATE: December 16, 1997
;   PRIOR FILING DATE: December 16, 1997
;   PRIOR APPLICATION NUMBER: 60/069,702
;   PRIOR FILING DATE: December 16, 1997
;   PRIOR APPLICATION NUMBER: 60/069,870
;   PRIOR FILING DATE: December 16, 1997
;   PRIOR APPLICATION NUMBER: 60/069,873
;   PRIOR FILING DATE: December 17, 1997
;   PRIOR APPLICATION NUMBER: 60/068,017
;   PRIOR FILING DATE: December 17, 1997
;   PRIOR APPLICATION NUMBER: 60/070,440
;   PRIOR FILING DATE: December 18, 1997
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Left column:
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;   PRIOR FILING DATE: February 25, 1998
;   PRIOR APPLICATION NUMBER: 60/112,850
;   PRIOR FILING DATE: December 16, 1998
;   PRIOR APPLICATION NUMBER: 60/113,296
;   PRIOR FILING DATE: December 22, 1998
;   PRIOR APPLICATION NUMBER: 60/146,222
;   PRIOR FILING DATE: July 28, 1999
;   PRIOR APPLICATION NUMBER: PCT/US98/19330
;   PRIOR FILING DATE: September 16, 1998
;   PRIOR APPLICATION NUMBER: PCT/US98/25108
;   PRIOR FILING DATE: December 1, 1998
;   PRIOR APPLICATION NUMBER: 09/216,021
;   PRIOR FILING DATE: December 16, 1998
;   PRIOR APPLICATION NUMBER: 09/218,517
;   PRIOR FILING DATE: December 22, 1998
;   PRIOR APPLICATION NUMBER: 09/254,311
;   PRIOR FILING DATE: March 3, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/12252
;   PRIOR FILING DATE: June 22, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/21090
;   PRIOR FILING DATE: September 15, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/28409
;   PRIOR FILING DATE: No. 6908993ember 30, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/28313
;   PRIOR FILING DATE: No. 6908993ember 30, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/28301
;   PRIOR FILING DATE: Decemberl, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/30095
;   PRIOR FILING DATE: December 16, 1999
;   PRIOR APPLICATION NUMBER: PCT/US00/03565
;   PRIOR FILING DATE: February 11, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/04414
;   PRIOR FILING DATE: February 22, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/05841
;   PRIOR FILING DATE: March 2, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/08439
;   PRIOR FILING DATE: March 30, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/14042
;   PRIOR FILING DATE: May 22, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/20710
;   PRIOR FILING DATE: July 28, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/32678
;   PRIOR FILING DATE: December 1, 2000
;   PRIOR APPLICATION NUMBER: PCT/US01/06520
;   PRIOR FILING DATE: February 28, 2001
;   NUMBER OF SEQ ID NOS: 120
SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien

Query Match       100.0%;   Score 3135;   DB 2;   Length 598;
Best Local Similarity 100.0%;   Pred. No. 7.3e-217;
Matches 598;    Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy    1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60

Qy   61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE 120

Qy  121 ALRLAGLGLQOLDEGLFSRLRNLHDLLDVSDNQLERVPPVIRGLTRLRLAGNTRIAQL 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ALRLAGLGLQOLDEGLFSRLRNLHDLLDVSDNQLERVPPVIRGLTRLRLAGNTRIAQL 180

Qy  181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE 240

Qy  241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    181  RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE  240
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Db    181  RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE  240

Qy    241  SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL  300
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL  300

Qy    301  APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG  360
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG  360

Qy    361  FTGLYCESQMGQGGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR  420
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  FTGLYCESQMGQGGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR  420

Qy    421  LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT  480
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT  480

Qy    481  PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV  540
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV  540

Qy    541  GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSGSECEVPLMGFPGPGLQSPLHAKPYI  598
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Db    541  GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSGSECEVPLMGFPGPGLQSPLHAKPYI  598
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RESULT 5
; Sequence 69, Application US/09945587
; Patent No. 6936254
; GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin
;   APPLICANT: Botstein,David
;   APPLICANT: Eaton,Dan
;   APPLICANT: Ferrara,Napoleone
;   APPLICANT: Filvaroff,Ellen
;   APPLICANT: Gerritsen,Mary
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul
;   APPLICANT: Grimaldi,Christopher
;   APPLICANT: Gurney,Austin
;   APPLICANT: Hillan,Kenneth
;   APPLICANT: Kljavin,Ivar
;   APPLICANT: Napier,Mary
;   APPLICANT: Roy,Margaret
;   APPLICANT: Tumas,Daniel
;   APPLICANT: Wood,William
;   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION: ACIDS ENCODING THE SAME
;   FILE REFERENCE: P2548P1C1
;   CURRENT APPLICATION NUMBER: US/09/945,587
;   CURRENT FILING DATE: 2001-09-26
;   PRIOR APPLICATION NUMBER: 09/866,028
;   PRIOR FILING DATE: 2001-05-25
;   PRIOR APPLICATION NUMBER: 60/067,411
;   PRIOR FILING DATE: December 3, 1997
;   PRIOR APPLICATION NUMBER: 60/069,334
;   PRIOR FILING DATE: December 11, 1997
;   PRIOR APPLICATION NUMBER: 60/069335
;   PRIOR FILING DATE: December 11, 1997
;   PRIOR APPLICATION NUMBER: 60/069,278
;   PRIOR FILING DATE: December 11, 1997
;   PRIOR APPLICATION NUMBER: 60/069,425
;   PRIOR FILING DATE: December 11, 1997
;   PRIOR APPLICATION NUMBER: 60/069,696
;   PRIOR FILING DATE: December 12, 1997
;   PRIOR APPLICATION NUMBER: 60/069,694
;   PRIOR FILING DATE: December 16, 1997
;   PRIOR APPLICATION NUMBER: 60/069,702
;   PRIOR FILING DATE: December 16, 1997
;   PRIOR APPLICATION NUMBER: 60/069,870
;   PRIOR FILING DATE: December 16, 1997

;   PRIOR FILING DATE: January 5, 1998
;   PRIOR APPLICATION NUMBER: 60/074,086
;   PRIOR FILING DATE: February 9, 1998
;   PRIOR APPLICATION NUMBER: 60/074,092
;   PRIOR FILING DATE: February 9, 1998
;   PRIOR APPLICATION NUMBER: 60/075,945
;   PRIOR FILING DATE: February 25, 1998
;   PRIOR APPLICATION NUMBER: 60/112,850
;   PRIOR FILING DATE: December 16, 1998
;   PRIOR APPLICATION NUMBER: 60/113,296
;   PRIOR FILING DATE: December 22, 1998
;   PRIOR APPLICATION NUMBER: 60/146,222
;   PRIOR FILING DATE: July 28, 1999
;   PRIOR APPLICATION NUMBER: PCT/US98/19330
;   PRIOR FILING DATE: September 16, 1998
;   PRIOR APPLICATION NUMBER: PCT/US98/25108
;   PRIOR FILING DATE: December 1, 1998
;   PRIOR APPLICATION NUMBER: 09/216,021
;   PRIOR FILING DATE: December 16, 1998
;   PRIOR APPLICATION NUMBER: 09/218,517
;   PRIOR FILING DATE: December 22, 1998
;   PRIOR APPLICATION NUMBER: 09/254,311
;   PRIOR FILING DATE: March 3, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/12252
;   PRIOR FILING DATE: June 22, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/21090
;   PRIOR FILING DATE: September 15, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/28409
;   PRIOR FILING DATE: No. 6929947ember 30, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/28313
;   PRIOR FILING DATE: No. 6929947ember 30, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/28301
;   PRIOR FILING DATE: December1, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/30095
;   PRIOR FILING DATE: December 16, 1999
;   PRIOR APPLICATION NUMBER: PCT/US00/03565
;   PRIOR FILING DATE: February 11, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/04414
;   PRIOR FILING DATE: February 22, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/05841
;   PRIOR FILING DATE: March 2, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/08439
;   PRIOR FILING DATE: March 30, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/14042
;   PRIOR FILING DATE: May 22, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/20710
;   PRIOR FILING DATE: July 28, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/32678
;   PRIOR FILING DATE: December 1, 2000
;   PRIOR APPLICATION NUMBER: PCT/US01/06520
;   PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
;
; SEQ ID NO 69
;   LENGTH: 598
;   TYPE: PRT
;   ORGANISM: Homo Sapien

Qy Query Match   100.0%; Score 3135; DB 2; Length 598;
    Best Local Similarity   100.0%; Pred. No. 7.3e-217;
    Matches 598; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MCSRVPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60
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Db   1 MCSRVPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60

Qy   61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE 120
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE 120

Qy   121 ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
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Db   61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  121 ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
Qy  181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE 240
Qy  241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
Qy  301 APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
Qy  361 FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR 420
Qy  421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT 480
Qy  481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV 540
Qy  541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI 598
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GPGAGPLELEGVVPLEPGPKATEGGGEALPSSECEVPLMGFPGPGLQSPLHAKPYI 598
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RESULT 6
; Sequence 69, Application US/09944884
; Patent No. 7018837
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,884
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien

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Query Match     100.0%;  Score 3135;  DB 3;  Length 598;
Best Local Similarity   100.0%;  Pred. No. 7.3e-217;
Matches  598;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1 MCSRVPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60
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; PRIOR FILING DATE:        December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE:        December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE:        December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE:        January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE:        February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE:        February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE:        February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE:        December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE:        December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE:        July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE:        September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE:        December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE:        December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE:        December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE:        March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE:        June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE:        September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE:        No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE:        No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE:        Decemberi, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE:        December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE:        February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE:        February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE:        March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE:        March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE:        May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE:        July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE:        December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE:        February 28, 2001
; NUMBER OF SEQ ID NOS:  120
; SEQ ID NO 69
; LENGTH:  598
; TYPE:  PRT
; ORGANISM:  Homo Sapien
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Query Match     100.0%;  Score 3135;  DB 2;  Length 598;
Best Local Similarity   100.0%;  Pred. No. 7.3e-217;
Matches  598;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1 MCSRVPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MCSRVPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60
Qy  61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE 120
        ||||||||||||||||||||||||||
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Db ||||||||||||||||||
Qy   1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSGCQSPQTVFCTARQGTTVPRDVPPDTVGLYVF 60
Db ||||||||||||||||||
Qy   61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLLDLSHNSLLALEPGILDTANVE 120
Db   61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLLDLSHNSLLALEPGILDTANVE 120
Qy   121 ALRLAGLGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
Db   121 ALRLAGLGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
Qy   181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE 240
Db   181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE 240
Qy   241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
Db   241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
Qy   301 APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
Db   301 APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
Qy   361 FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR 420
Db   361 FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR 420
Qy   421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT 480
Db   421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT 480
Qy   481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV 540
Db   481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV 540
Qy   541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSGSECEVPLMGFPGPGLQSPLHAKPYI 598
Db   541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSGSECEVPLMGFPGPGLQSPLHAKPYI 598

Db   121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLLDLSHNS 180
Qy   106 LLALEPGILDTANVEALRLAGLGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 165
Db   181 LLALEPGILDTANVEALRLAGLGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 240
Qy   166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLLAAARNPF 225
Db   241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 300
Qy   226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
Db   301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT 360
Qy   286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC 345
Db   361 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC 420
Qy   346 HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGL 405
Db   421 HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGL 480
Qy   406 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP 465
Db   481 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP 540
Qy   466 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 525
Db   541 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 600
Qy   526 RGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSGSECEVPLMGFPG 585
Db   601 RGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSGSECEVPLMGFPG 660
Qy   586 PGLQSPLHAKPYI 598
Db   661 PGLQSPLHAKPYI 673

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; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-063-950-2

Query Match   98.4%; Score 3083.5; DB 2; Length 673;
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Matches 597; Conservative   0; Mismatches   1; Indels   75; Gaps   1;

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J.Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787

us-10-677-669-69.rai.spd1

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;, PRIOR FILING DATE: 1998-07-07
;, PRIOR APPLICATION NUMBER: 60/092182
;, PRIOR FILING DATE: 1998-07-09
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; Patent No. 6930170
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT: Baker,Kevin P.
;  APPLICANT: Botstein,David
;  APPLICANT: Desnoyers,Luc
;  APPLICANT: Eaton,Dan L.
;  APPLICANT: Ferrara,Napoleone
;  APPLICANT: Fong,Sherman
;  APPLICANT: Gerber,Hanspeter
;  APPLICANT: Gerritsen,Mary E.
;  APPLICANT: Goddard,Audrey
;  APPLICANT: Godowski,Paul J.
;  APPLICANT: Grimaldi,J.Christopher
;  APPLICANT: Gurney,Austin L.
;  APPLICANT: Kljavin,Ivar J.
;  APPLICANT: Napier,Mary A.
;  APPLICANT: Pan,James
;  APPLICANT: Paoni,Nicholas F.
;  APPLICANT: Roy, Margaret Ann
;  APPLICANT: Stewart, Timothy A.
;  APPLICANT: Tumas, Daniel
;  APPLICANT: Watanabe, Colin K.
;  APPLICANT: Williams, P. Mickey
;  APPLICANT: Wood, William I.
;  APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE:   2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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Best Local Similarity   88.7%;    Pred. No. 4.2e-213;
Matches  597;  Conservative    0;   Mismatches   1;   Indels  75;   Gaps    1;

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Db     1 MCSRVPLLLLPLLLLALGPGVQGCPSGCQSQPQTVFCTARQGTTVPRDVPPDTVGLYVF  60

Qy    61 ENGITMLDASSFAGLPGLQLLDLSQNQIAS------------------------------  90
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Db    61 ENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120

Qy    91 ------------------------------------------LRLPRLLLLDLSHNS 105
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Db   121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNS 180

Qy   106 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 240

Qy   166 LTRLRLAGNTRIAQLRPEDLAGLAALAQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 225
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LTRLRLAGNTRIAQLRPEDLAGLAALAQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 300

Qy   226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLELDYADFGCPATTTTATVPT 285
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Qy   286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPODCPPSTCLNGGTC 345
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Qy   406 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP 465
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Qy   466 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGRAYCVR 525
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
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Query Match          98.4%;    Score 3083.5;   DB 2;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 4.2e-213;
Matches   597;  Conservative   0;  Mismatches   0;  Indels  75;  Gaps  1;

Qy    1 MCSRVPLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60
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Db    1 MCSRVPLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60

Qy   61 ENGITMLDASSFAGLPGLQLLDLSQNQIAS------------------------------ 90
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Db   61 ENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120

Qy   91 ------------------------------------------LRLPRLLLLDLSHNS 105
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Db  121 RGLRLRERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPLPRLRLPRLLLLDLSHNS 180
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Qy   106  LLALEPGILDTANVEALRLAGLGLGLGQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG  165
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Db   181  LLALEPGILDTANVEALRLAGLGLGLGQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG  240

Qy   166  LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF    225
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Db   241  LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF    300

Qy   226  NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT    285
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Db   301  NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT    360

Qy   286  TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC    345
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Db   361  TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC    420

Qy   346  HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGL   405
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Db   421  HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGL   480

Qy   406  QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP   465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP   540

Qy   466  GRVPEGGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR  525
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GRVPEGGEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR   600

Qy   526  RGRAMAAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG  585
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Db   601  RGRAMAAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG  660

Qy   586  PGLQSPLHAKPYI  598
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Db   661  PGLQSPLHAKPYI  673
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RESULT 10
; Sequence 52, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
;   APPLICANT: Ashkenazi,Avi J.
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Botstein,David
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Eaton,Dan L.
;   APPLICANT: Ferrara,Napoleone
;   APPLICANT: Fong,Sherman
;   APPLICANT: Gerber,Hanspeter
;   APPLICANT: Gerritsen,Mary E.
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Grimaldi,J.Christopher
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Kljavin,Ivar J.
;   APPLICANT: Napier,Mary A.
;   APPLICANT: Pan,James
;   APPLICANT: Paoni,Nicholas F.
;   APPLICANT: Roy,Margaret Ann
;   APPLICANT: Stewart,Timothy A.
;   APPLICANT: Tumas,Daniel
;   APPLICANT: Watanabe,Colin K.
;   APPLICANT: Williams, P. Mickey
;   APPLICANT: Wood, William I.
;   APPLICANT: Zhang,Zemin
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION: Acids Encoding the Same
;   FILE REFERENCE: P2730P1C27
;   CURRENT APPLICATION NUMBER: US/09/997,333
;   CURRENT FILING DATE: 2001-11-15
;   PRIOR APPLICATION NUMBER: 60/049787
;   PRIOR FILING DATE: 1997-06-16

;   PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Query Match          98.4%;   Score 3083.5;   DB 2;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 4.2e-213;
Matches  597;  Conservative  0;  Mismatches  1;  Indels  75;  Gaps  1;

Qy    1 MCSRVPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MCSRVPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF   60

Qy   61 ENGITMLDASSFAGLPGLQLDLSQNQIAS---------                       90
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Db   61 ENGITMLDAGSFAGLPGLQLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120

Qy   91 --------------------------LRLPRLLLLDLSHNS                   105
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Db  121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNS 180

Qy  106 LLALEPGILDTANVEALRLAGLGLQOLDEGLFSRLRNLHDLVSDNQLERVPPVIRGLRG 165
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LLALEPGILDTANVEALRLAGLGLQOLDEGLFSRLRNLHDLVSDNQLERVPPVIRGLRG 240

Qy  166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 225
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 300

Qy  226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
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Qy  286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPDCPPSTCLNGGTC 345
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Qy  466 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 525
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Qy  526 RGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG 585
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Qy  586 PGLQSPLHAKPYI                                               598
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Db  661 PGLQSPLHAKPYI                                               673
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26

RESULT 11
; Sequence 52, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; ,, APPLICANT: Ashkenazi,Avi J.
; ,, APPLICANT: Baker,Kevin P.
; ,, APPLICANT: Botstein,David
; ,, APPLICANT: Desnoyers,Luc
; ,, APPLICANT: Eaton,Dan L.
; ,, APPLICANT: Ferrara,Napoleone
; ,, APPLICANT: Fong,Sherman
; ,, APPLICANT: Gerber,Hanspeter
; ,, APPLICANT: Gerritsen,Mary E.
; ,, APPLICANT: Goddard,Audrey
; ,, APPLICANT: Godowski,Paul J.
; ,, APPLICANT: Grimaldi,J.Christopher
; ,, APPLICANT: Gurney,Austin L.
; ,, APPLICANT: Kljavin,Ivar J.
; ,, APPLICANT: Napier,Mary A.
; ,, APPLICANT: Pan,James
; ,, APPLICANT: Paoni,Nicholas F.
; ,, APPLICANT: Roy, Margaret Ann
; ,, APPLICANT: Stewart, Timothy A.
; ,, APPLICANT: Tumas,Daniel
; ,, APPLICANT: Watanabe, Colin K.
; ,, APPLICANT: Williams, P. Mickey
; ,, APPLICANT: Wood, William I.
; ,, APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Qy  226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
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Qy  286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC 345
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RESULT 12
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; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C61
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Query Match   98.4%; Score 3083.5; DB 2; Length 673;
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;   PRIOR FILING DATE: 1998-07-07
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;   PRIOR FILING DATE: 1998-07-09
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;  GENERAL INFORMATION:
..  APPLICANT: Ashkenazi,Avi J.
..  APPLICANT: Baker,Kevin P.
..  APPLICANT: Botstein,David
..  APPLICANT: Desnoyers,Luc
..  APPLICANT: Eaton,Dan L.
..  APPLICANT: Ferrara,Napoleone
..  APPLICANT: Fong,Sherman
..  APPLICANT: Gerber,Hanspeter
..  APPLICANT: Gerritsen,Mary E.
..  APPLICANT: Goddard,Audrey
..  APPLICANT: Godowski,Paul J.
..  APPLICANT: Grimaldi,J.Christopher
..  APPLICANT: Gurney,Austin L.
..  APPLICANT: Kljavin,Ivar J.
..  APPLICANT: Napier,Mary A.
..  APPLICANT: Pan,James
..  APPLICANT: Paoni,Nicholas F.
..  APPLICANT: Roy, Margaret Ann
..  APPLICANT: Stewart, Timothy A.
..  APPLICANT: Tumas,Daniel
..  APPLICANT: Watanabe, Colin K.
..  APPLICANT: Williams, P. Mickey
..  APPLICANT: Wood, William I.
..  APPLICANT: Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION: Acids Encoding the Same
;  FILE REFERENCE: P2730P1C60
;  CURRENT APPLICATION NUMBER: US/09/989,726
;  CURRENT FILING DATE:  2001-11-19
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Best Local Similarity  88.7%;   Pred. No. 4.2e-213;
Matches 597; Conservative  0; Mismatches  0; Indels  1; Gaps  1;

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PRIOR FILING DATE: 1998-07-09
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Query Match             98.4%;   Score 3083.5;   DB 3;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 4.2e-213;
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Db    1 MCSRVPLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60

Qy   61 ENGITMLDASSFAGLPGLQLLDLSQNQIAS--------------------------- 90
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Qy   91 --------------------------------------------LRLPRLLLLDLSHNS 105
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Qy  106 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 165
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Db   181 ||||||||||||||||||||||||||||
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Qy   166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 225
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Qy   226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
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Db   301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT 360

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Qy   586 PGLQSPLHAKPYI 598
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Zhang, Zemin
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PRIOR FILING DATE: 1998-07-07 PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 88.7%;     Pred. No. 4.2e-213;
Matches  597;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

Qy    1 MCSRVPLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60
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Db    1 MCSRVPLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60

Qy   61 ENGITMLDASSFAGLPGLQLDLSQNQIAS---------------------- 90
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Db   61 ENGITMLDAGSFAGLPGLQLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120

Qy   91 ---------------LRLPRLLLLDLSHNS 105
                         |||||||||||||||
Db  121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNS 180

Qy  106 LLALEPGLLDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 165
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LLALEPGLLDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 240

Qy  166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 225
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Db  241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 300

Qy  226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
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Db  301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT 360

Qy  286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC 345
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Qy  346 HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGL 405
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Qy  406 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP 465
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Qy  466 GRVPEGEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 525
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Qy  586 PGLQSPLHAKPYI 598
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Db  661 PGLQSPLHAKPYI 673
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Sequence 52, Application US/09989728
Patent No. 7029873
GENERAL INFORMATION:
APPLICANT: Ashkenazi,Avi J.
APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
APPLICANT: Desnoyers,Luc
APPLICANT: Eaton,Dan L.
APPLICANT: Ferrara,Napoleone
APPLICANT: Fong,Sherman
APPLICANT: Gerber,Hanspeter
APPLICANT: Gerritsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Godowski,Paul J.
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Gurney,Austin L.
APPLICANT: Kljavin,Ivar J.
APPLICANT: Napier,Mary A.
APPLICANT: Pan,James
APPLICANT: Paoni,Nicholas F.
APPLICANT: Roy,Margaret Ann
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K.
APPLICANT: Williams,P.Mickey
APPLICANT: Wood,William I.
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C72
CURRENT APPLICATION NUMBER: US/09/989,728
CURRENT FILING DATE: 2001-11-20
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091626
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Db  181 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 240

Qy  166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 225
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Db  241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 300

Qy  226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
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Db  301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT 360

Qy  286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC 345
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Qy  346 HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGL 405
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Db  421 HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGL 480

Qy  406 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP 465
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Db  481 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP 540

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Qy  586 PGLQSPLHAKPYI 598
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Db  661 PGLQSPLHAKPYI 673
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Search completed: January 28, 2007, 17:27:08
Job time : 73 secs

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Best Local Similarity   88.7%;  Pred. No. 4.2e-213;
Matches  597;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

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Db    1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60

Qy   61 ENGITMLDASSFAGLPGLQLDLSQNQIAS------------------------------- 90
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Db   61 ENGITMLDDAGSFAGLPGLQLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120

Qy   91 -------------------------------------LRLPRLLLLDLSHNS 105
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Db  121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNS 180

Qy  106 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 165
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                    GenCore version 6.2
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OM protein - protein search, using sw model

Run on:   January 28, 2007, 17:48:32 ; Search time 190 Seconds
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Title:           US-10-677-669-69
Perfect score:   3135
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Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters:    2097797

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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126	3135	100.0	598	4	US-10-677-471-69	Sequence 69, Appl
127	3135	100.0	598	4	US-10-677-660-69	Sequence 69, Appl
129	3135	100.0	598	5	US-10-735-014-69	Sequence 69, Appl
130	3135	100.0	598	5	US-10-854-947-69	Sequence 69, Appl
131	3135	100.0	598	5	US-10-858-993-69	Sequence 69, Appl
133	3135	100.0	598	5	US-10-901-400-69	Sequence 69, Appl
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135	3135	100.0	598	5	US-10-889-671-69	Sequence 69, Appl
136	3135	100.0	598	5	US-10-943-353-69	Sequence 69, Appl
143	3083.5	98.4	673	3	US-09-782-980-59	Sequence 59, Appl
169	3083.5	98.4	673	3	US-09-997-428-52	Sequence 52, Appl
270	3083.5	98.4	673	4	US-10-063-742-16	Sequence 16, Appl
363	3083.5	98.4	673	4	US-10-806-018-59	Sequence 59, Appl
364	3083.5	98.4	673	5	US-10-972-317-16	Sequence 16, Appl
365	3083.5	98.4	673	5	US-10-950-374-52	Sequence 52, Appl
367	3083.5	98.4	673	6	US-11-102-240-16	Sequence 16, Appl
368	3083.5	98.4	673	6	US-11-103-195-16	Sequence 16, Appl
369	3078.5	98.2	676	4	US-10-029-386-33083	Sequence 33083, A
370	2935	93.6	672	4	US-10-050-704-99	Sequence 99, Appl
371	2935	93.6	672	4	US-10-798-512-99	Sequence 99, Appl
372	2935	93.6	723	4	US-10-050-704-186	Sequence 186, App
373	2935	93.6	723	4	US-10-798-512-186	Sequence 186, App
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376	2484	79.2	673	4	US-10-487-421-10	Sequence 10, Appl
377	1178.5	37.6	281	3	US-09-866-050A-648	Sequence 648, App
378	980.5	31.3	307	5	US-10-491-355-18	Sequence 18, Appl
379	360.5	11.5	635	5	US-10-363-374-8	Sequence 8, Appli
380	360.5	11.5	647	4	US-10-093-463-188	Sequence 188, App
381	357.5	11.4	778	4	US-10-093-463-192	Sequence 192, App
382	339	10.8	566	4	US-10-093-463-190	Sequence 190, App
383	338	10.8	551	3	US-09-897-214-8	Sequence 8, Appli
384	337	10.7	653	3	US-09-957-187-10	Sequence 10, Appl
385	337	10.7	653	6	US-11-058-709-10	Sequence 10, Appl
386	333	10.6	590	3	US-09-957-187-12	Sequence 12, Appl
387	333	10.6	590	6	US-11-058-709-12	Sequence 12, Appl
388	332	10.6	526	3	US-10-450-763-35186	Sequence 35186, A
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905	330	10.5	653	5	US-10-931-886-438	Sequence 438, App
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908	330	10.5	653	5	US-10-950-374-229	Sequence 229, App
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915	330	10.5	653	5	US-11-135-855-25	Sequence 25, Appl
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919	329	10.5	649	5	US-10-028-392-58	Sequence 58, Appl
928	328.5	10.5	627	4	US-10-237-535-100	Sequence 100, App
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Job time : 220 secs
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OM protein - protein search, using sw model

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Scoring table: BLOSUM62
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Searched: 507816 seqs, 12256O497 residues

Total number of hits satisfying chosen parameters: 507816

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
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5	3083.5	98.4	673	7	US-11-371-354-70967	Sequence 70967, A
6	3083.5	98.4	673	7	US-11-102-284-16	Sequence 16, Appl
7	3078.5	98.2	673	7	US-11-090-997-1750	Sequence 1750, Ap
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9	2935	93.6	672	7	US-11-366-486-817	Sequence 817, APP
10	2490	79.4	673	7	US-11-090-997-528	Sequence 528, App
11	359.5	11.5	635	7	US-11-371-354-63559	Sequence 63559, A
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14	322.5	10.3	811	6	US-10-505-928-87	Sequence 87, Appl
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17	320	10.2	660	7	US-11-240-891-115	Sequence 115, Appl
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19	313.5	10.0	656	7	US-11-030-653-38	Sequence 38, Appl
20	312	10.0	592	6	US-10-486-020-19	Sequence 19, Appl
21	312	10.0	592	7	US-11-030-653-14	Sequence 14, Appl
24	309	9.9	649	7	US-11-101-316-132	Sequence 132, App
25	309	9.9	649	7	US-11-376-673-132	Sequence 132, App
26	309	9.9	649	7	US-11-102-284-132	Sequence 132, App
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28	308	9.8	649	6	US-10-219-051B-7172	Sequence 7172, Ap
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73	251	8.0		US-10-405-027-5755	6	Sequence 5755, Ap
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86	230	7.3		US-11-429-276-1659	7	Sequence 1659, Ap
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88	227.5	7.3		US-11-293-697-3841	7	Sequence 3841, Ap
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117	211	6.7	513	7	US-11-102-284-124	Sequence 124, App
118	211	6.7	531	7	US-11-257-581-5	Sequence 5, Appli
119	211	6.7	531	7	US-11-257-581-4	Sequence 4, Appli
120	210	6.7	531	7	US-11-257-579-5	Sequence 5, Appli
121	210	6.7	531	7	US-11-257-579-4	Sequence 4, Appli
122	209	6.7	1091	6	US-11-219-051B-5403	Sequence 5403, A
123	208.5	6.7	382	7	US-11-371-354-62135	Sequence 62135, A
124	208.5	6.7	507	7	US-11-214-063A-954	Sequence 954, App
125	206	6.6	353	7	US-11-371-354-55463	Sequence 55463, A
127	206	6.6	428	6	US-10-405-027-5521	Sequence 5521, Ap
128	206	6.6	428	6	US-10-405-027-5523	Sequence 5523, Ap
129	206	6.6	428	7	US-10-240-081-17	Sequence 17, Appl
130	205.5	6.6	578	7	US-11-214-063A-1256	Sequence 1256, Ap
131	205	6.5	740	7	US-11-371-354-60445	Sequence 60445, A
132	204.5	6.5	557	7	US-11-030-653-12	Sequence 12, Appl
133	203.5	6.5	513	7	US-11-214-063A-1258	Sequence 1258, Ap
134	203.5	6.5	4303	7	US-11-485-062-2	Sequence 2, Appli
135	202	6.4	472	7	US-11-214-063A-1334	Sequence 1334, Ap
136	201.5	6.4	606	7	US-11-166-372-2513	Sequence 2513, Ap
137	200.5	6.4	295	6	US-11-166-356-1193	Sequence 1193, Ap
138	200.5	6.4	295	6	US-10-664-356-654	Sequence 654, App
139	200.5	6.4	302	6	US-10-664-356-1679	Sequence 1679, Ap
140	200.5	6.4	302	6	US-10-664-356-925	Sequence 925, App
141	200.5	6.4	302	6	US-11-366-486-925	Sequence 106, App
142	199	6.3	256	7	US-11-214-063A-946	Sequence 946, App
143	197.5	6.3	256	6	US-10-405-027-3896	Sequence 3896, Ap
144	197.5	6.3	548	6	US-10-486-020-2	Sequence 2, Appli
147	195.5	6.2	423	7	US-11-030-653-28	Sequence 28, Appl
149	195	6.2	620	7	US-11-030-653-73	Sequence 73, Appl
150	195	6.2	837	7	US-11-371-354-66139	Sequence 66139, A
151	194	6.2	314	7	US-11-520-715-50825	Sequence 50825, A
152	193.5	6.2	545	7	US-10-030-653-6	Sequence 6, Appli
153	193	6.2	40	7	US-11-134-871-3226	Sequence 3226, Ap
154	192.5	6.2	967	7	US-11-500-008-2	Sequence 2, Appli
155	190	6.1	1059	6	US-10-970-823-290	Sequence 290, App
157	190	6.1	1119	6	US-10-970-823-294	Sequence 294, App
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159	189.5	6.0	301	7	US-11-257-579-9	Sequence 9, Appli
160	189	6.0	369	6	US-10-219-051B-8199	Sequence 8199, Ap
161	186.5	5.9	633	6	US-11-511-141-9	Sequence 9, Appli
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163	186.5	5.9	839	7	US-11-301-373-61	Sequence 61, Appl
164	186	5.9	839	7	US-11-399-274-1	Sequence 1, Appli
165	186	5.9	894	7	US-11-343-271-49	Sequence 49, Appli
166	186	5.9	379	7	US-11-371-354-55735	Sequence 55735, A
167	185	5.9	379	7	US-11-030-653-36	Sequence 36, Appl
168	184	5.8	381	6	US-11-257-581-7	Sequence 7, Appli
169	184	5.8	290	7	US-10-505-928-743	Sequence 743, App
170	184	5.8	368	6	US-11-371-354-73127	Sequence 73127, A
171	183	5.8	662	6	US-10-528-260B-145	Sequence 145, A
172	183	5.8	662	6	US-11-371-354-70965	Sequence 70965, A
173	182.5	5.7	379	6	US-11-296-092-2	Sequence 2, Appli
175	182.5	5.7	379	7	US-11-296-155-2	Sequence 2, Appli
176	182.5	5.7	381	7	US-10-527-101-4	Sequence 4, Appli
177	179	5.7	290	7	US-11-257-581-10	Sequence 10, Appl
178	179	5.7	290	7	US-11-257-581-11	Sequence 11, Appl
179	179	5.7	290	7	US-11-257-581-12	Sequence 12, Appl
180	179	5.7	290	7	US-11-257-579-10	Sequence 10, Appl
181	179	5.7	290	7	US-11-257-579-11	Sequence 11, Appl
182	179	5.7	290	7	US-11-257-579-12	Sequence 12, Appl
183	179	5.7	302	7	US-11-257-581-8	Sequence 8, Appli
184	178.5	5.7	493	6	US-11-257-579-8	Sequence 8, Appli
185	178	5.7	522	7	US-11-166-372-2689	Sequence 2689
186	178	5.7	1043	6	US-11-387-182-2	Sequence 205, App
188	178	5.7	1049	6	US-10-528-260B-205	Sequence 205, App
189	178	5.7	1049	7	US-11-368-333-24	Sequence 24, Appl
191	177.5	5.7	1049	6	US-11-368-334-18	Sequence 18, Appl
192	177	5.7	1049	7	US-11-387-182-4	Sequence 4, Appli
193	178	5.7	1049	7	US-11-368-333-26	Sequence 26, Appl
194	178	5.7	1049	7	US-11-387-182-4	Sequence 4, Appli
195	177.5	5.7	1050	7	US-11-368-333-26	Sequence 26, Appl
196	177.5	5.7	1050	7	US-11-368-334-22	Sequence 22, Appl

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206	175	5.6	591	7	US-11-511-141-4	Sequence 4, Appl1
207	175	5.6	951	6	US-11-511-141-2	Sequence 2, Appl1
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213	172.5	5.5	359	6	US-10-219-051B-9723	Sequence 9723, Ap
214	172.5	5.5	359	6	US-10-219-051B-9727	Sequence 9727, Ap
215	172.5	5.5	359	6	US-10-219-051B-9731	Sequence 9731, Ap
216	172.5	5.5	359	6	US-10-219-051B-9735	Sequence 9735, Ap
217	172.5	5.5	1388	6	US-10-219-051B-9739	Sequence 9739, Ap
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221	170.5	5.4	907	6	US-10-533-519-36	Sequence 36, Appl
222	170	5.4	907	6	US-10-570-909-115	Sequence 115, App
223	170	5.4	907	6	US-10-541-749-141	Sequence 141, App
224	170	5.4	907	6	US-10-219-051B-5041	Sequence 5041, Ap
225	170	5.4	907	7	US-10-219-051B-5044	Sequence 5044, Ap
226	170	5.4	1038	6	US-11-486-332-10	Sequence 10, Appl
227	169.5	5.4	73	6	US-10-539-228-157	Sequence 157, App
228	168.5	5.4	907	6	US-10-539-228-160	Sequence 160, App
229	168.5	5.4	977	7	US-11-486-332-11	Sequence 11, Appl
230	168	5.4	794	6	US-11-511-141-10	Sequence 10, Appl
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232	166.5	5.3	544	7	US-10-449-902-37455	Sequence 37455, A
233	166.5	5.3	546	6	US-10-664-356-1680	Sequence 1680, Ap
234	166.5	5.3	549	7	US-11-366-486-926	Sequence 926, App
235	166.5	5.3	549	7	US-11-375-555-175	Sequence 175, App
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243	166	5.3	736	7	US-11-134-871-3225	Sequence 3225, Ap
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245	166	5.3	885	6	US-11-612-783-6596	Sequence 6596, Ap
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254	165	5.2	501	6	US-10-970-823-185	Sequence 185, App
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258	164	5.2	611	7	US-10-449-902-36779	Sequence 36779, A
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262	164	5.2	736	7	US-11-291-140-4	Sequence 4, Appli
263	164	5.2	904	6	US-11-500-008-8	Sequence 8, Appli
264	164	5.2	904	6	US-11-144-322-2	Sequence 2, Appli
265	164	5.2	915	6	US-11-291-140-2	Sequence 20, Appl
266	164	5.2	915	6	US-11-368-333-20	Sequence 2, Appli
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268	164	5.2	2000	6	US-10-540-808-3	Sequence 3, Appli
269	164	5.2	2026	6	US-11-500-008-11	Sequence 11, Appl
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278	163	5.2	753	7	US-11-129-648-13	Sequence 13, Appl
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319	156	5.0	354	6	US-10-219-051B-9733	Sequence 9733, Ap
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1451	112	3.6	246	6	US-11-056-355B-18175	Sequence 18175, A
1452	112	3.6	275	7	US-11-056-355B-59359	Sequence 59359, A
1453	112	3.6		6	US-10-953-349-18174	Sequence 18174, A
1454	112	3.6		6	US-11-056-355B-59358	Sequence 59358, A
1455	112	3.6		7	US-11-056-355B-22076	Sequence 22076, A

1457	112	3.6	279	6	US-10-533-519-2317	Sequence 2317, Ap
1458	112	3.6	293	7	US-11-056-355B-22075	Sequence 22075, A
1459	112	3.6	310	6	US-10-570-909-7	Sequence 7, Appli
1460	112	3.6	318	6	US-10-953-349-27976	Sequence 27976, A
1461	112	3.6	318	7	US-11-056-355B-69074	Sequence 69074, A
1462	112	3.6	334	6	US-10-953-349-27975	Sequence 27975, A
1463	112	3.6	334	7	US-11-056-355B-69073	Sequence 69073, A
1464	112	3.6	355	6	US-10-953-349-27974	Sequence 27974, A
1465	112	3.6	355	7	US-11-056-355B-69072	Sequence 69072, A
1466	112	3.6	383	6	US-10-953-349-16918	Sequence 16918, A
1467	112	3.6	383	6	US-10-570-909-118	Sequence 118, App
1468	112	3.6	383	7	US-11-371-354-73975	Sequence 73975, A
1469	112	3.6	404	7	US-11-166-372-3089	Sequence 3089, Ap
1470	112	3.6	542	6	US-10-449-902-42550	Sequence 42550, A
1471	112	3.6	641	6	US-10-449-902-47052	Sequence 47052, A
1472	112	3.6	731	7	US-11-056-355B-80297	Sequence 80297, A
1473	112	3.6	764	7	US-11-232-404-75	Sequence 75, Appl
1474	112	3.6	764	7	US-11-404-939-395	Sequence 395, App
1475	112	3.6	764	7	US-11-404-939-399	Sequence 399, App
1476	112	3.6	764	7	US-11-404-939-403	Sequence 403, App
1477	112	3.6	764	7	US-11-404-939-407	Sequence 407, App
1478	112	3.6	764	7	US-11-404-939-411	Sequence 411, App
1479	112	3.6	764	7	US-11-404-939-415	Sequence 415, App
1480	112	3.6	764	7	US-11-404-939-419	Sequence 419, App
1481	112	3.6	764	7	US-11-404-939-423	Sequence 423, App
1482	112	3.6	764	7	US-11-188-417A-92	Sequence 92, Appl
1483	112	3.6	785	6	US-10-537-228A-63	Sequence 63, Appl
1484	112	3.6	864	7	US-11-178-724-27	Sequence 27, Appl
1485	112	3.6	864	6	US-11-188-417A-98	Sequence 98, Appl
1486	112	3.6	864	7	US-11-231-494-34	Sequence 34, Appl
1487	112	3.6	883	6	US-10-219-051B-8512	Sequence 8512, Ap
1488	112	3.6	894	7	US-11-389-343-1119	Sequence 1119, Ap
1489	112	3.6	894	7	US-11-389-017-1119	Sequence 1119, Ap
1490	112	3.6	902	7	US-11-371-354-67529	Sequence 67529, A
1491	112	3.6	902	7	US-11-371-354-77063	Sequence 77063, A
1492	112	3.6	932	7	US-11-371-354-59621	Sequence 59621, A
1493	112	3.6	1014	7	US-11-056-355B-72514	Sequence 72514, A
1494	112	3.6	1015	7	US-11-056-355B-72513	Sequence 72513, A
1495	112	3.6	1019	7	US-11-056-355B-72512	Sequence 72512, A
1496	112	3.6	1066	6	US-10-449-902-43289	Sequence 43289, A
1497	111.5	3.6	273	7	US-11-520-715-52861	Sequence 52861, A
1498	111.5	3.6	315	6	US-10-953-349-26294	Sequence 26294, A
1499	111.5	3.6	315	7	US-11-056-355B-62479	Sequence 62479, A
1500	111.5	3.6	412	7	US-11-371-354-64155	Sequence 64155, A

Search completed: January 28, 2007, 17:54:36
Job time : 70 secs

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GenCore version 6.2

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OM protein - protein search, using sw model

Run on: January 28, 2007, 17:27:21 ; Search time 346 Seconds
          (without alignments)
          1852.978 Million cell updates/sec

Title: US-10-677-669-69
Perfect score: 3135
Sequence: 1 MCSRVPLLPLLLLLALGPG..........PLMGFPGPGLQSPLHAKPYI 598

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs; 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :   UniProt_8.4:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3078.5	98.2	673	1	VASN_HUMAN	Q6emk4 homo sapien
2	2490	79.4	673	1	VASN_MOUSE	Q9czt5 mus musculu
3	1213.5	38.7	661	1	VASN_XENTR	Q6df55 xenopus tro
4	972.5	31.0	688	2	Q3MKM9_BRARE	Q3mkm9 brachydanio
5	927.5	29.6	643	2	Q503G2_BRARE	Q503g2 brachydanio
6	914.5	29.2	962	2	Q4SQ68_TETNG	Q4sq68 tetraodon n
7	368.5	11.8	513	1	LRRC4_HUMAN	Q50lg9 homo sapien
8	359.5	11.5	635	1	LRFN4_HUMAN	Q6pjg9 homo sapien
9	351	11.2	636	1	LRFN4_MOUSE	Q80xu8 mus musculu
10	348	11.1	636	2	Q460G5_MOUSE	Q460g5 mus musculu
11	341	10.9	634	2	Q3UVS6_MOUSE	Q3uvs6 mus musculu
12	341	10.9	660	2	Q8BLU0_MOUSE	Q8blu0 m adult mal
13	339	10.8	521	1	LRC24_MOUSE	Q8bha1 mus musculu
14	338	10.8	655	2	Q4SGV9_TETNG	Q4sgv9 tetraodon n
15	332	10.6	637	2	Q6A073_MOUSE	Q6a073 mus musculu
16	331.5	10.6	622	2	Q59GV4_HUMAN	Q59gv4 homo sapien
17	330	10.5	653	1	LRRC4_HUMAN	Q9hbw1 homo sapien
18	329.5	10.5	648	2	Q6DDY0_XENLA	Q6ddy0 xenopus lae
19	325.5	10.4	570	2	Q70AK2_XENLA	Q70ak2 xenopus lae
20	324	10.3	626	1	LRFN3_MOUSE	Q8bly3 mus musculu
21	324	10.3	626	2	Q505E2_MOUSE	Q505e2 mus musculu
22	323	10.3	732	2	Q4RPB8_TETNG	Q4rpb8 tetraodon n
23	322.5	10.3	682	2	Q6DJD2_XENLA	Q6djd2 xenopus lae
24	322.5	10.3	811	2	Q7L0X0_HUMAN	Q710x0 homo sapien
25	322.5	10.3	887	2	O75139_HUMAN	O75139 homo sapien
26	322	10.3	605	1	ALS_PAPHA	O02833 papio hamad
27	321.5	10.2	709	1	LRC4B_MOUSE	P0c192 mus musculu
28	321	10.2	628	1	LRFN3_HUMAN	Q9btn0 homo sapien
29	321	10.2	762	2	Q5JY13_HUMAN	Q5jy13 homo sapien
30	320.5	10.2	597	2	Q3I0Y3_BOVIN	Q3i0y3 bos taurus
31	320	10.2	660	1	FLRT2_HUMAN	O43155 homo sapien
32	320	10.2	674	2	Q6RKD8_MOUSE	Q6rkd8 m fibronect
33	319	10.2	602	2	Q58CS0_BOVIN	Q58cs0 bos taurus
34	319	10.2	652	2	Q45R42_RAT	Q45r42 rattus norv
35	318.5	10.2	652	1	LRRC4_MOUSE	Q99ph1 mus musculu
36	317	10.1	778	1	Q6NUI6_HUMAN	Q6nui6 homo sapien
37	316.5	10.1	713	1	LRC4B_HUMAN	Q9nt99 homo sapien
38	313	10.0	628	2	Q1RMS4_BOVIN	Q1rms4 bos taurus
39	312.5	10.0	648	2	Q70AK3_XENLA	Q70ak3 xenopus lae
40	312.5	10.0	935	2	Q4SBT7_TETNG	Q4sbt7 tetraodon n
41	311.5	9.9	420	1	R4RL2_MOUSE	Q7m6z0 mus musculu
42	310.5	9.9	420	1	R4RL2_RAT	Q80wd1 rattus norv
43	310.5	9.9	646	1	FLRT1_HUMAN	Q9nzu1 homo sapien
44	308	9.8	627	2	Q8NC95_HUMAN	Q8nc95 homo sapien
45	308	9.8	649	1	FLRT3_HUMAN	Q9nzu0 homo sapien
46	308	9.8	649	2	Q54ZZ9_HUMAN	Q54zz9 homo sapien
47	307.5	9.8	626	2	Q4TBM8_TETNG	Q4tbm8 tetraodon n
48	307.5	9.8	674	2	Q8WVA2_HUMAN	Q8wva2 homo sapien
49	307	9.8	637	2	Q68F21_XENLA	Q68f21 xenopus lae
50	307	9.8	649	2	Q5R6T0_PONPY	Q5r6t0 pongo pygma
51	306.5	9.8	649	2	Q6PHP6_MOUSE	Q6php6 mus musculu
52	305.5	9.7	730	2	Q6US92_MOUSE	Q6us92 mus musculu
53	303.5	9.7	692	2	Q4GOS0_HUMAN	Q4g0s0 homo sapien
54	302.5	9.6	420	1	R4RL2_HUMAN	Q86un3 homo sapien
55	302.5	9.6	420	2	Q17RL9_HUMAN	Q17rl9 homo sapien
56	302.5	9.6	618	2	Q4SHD7_TETNG	Q4shd7 tetraodon n
57	302	9.6	605	1	ALS_HUMAN	P35858 homo sapien
58	302	9.6	605	2	Q8TAY0_HUMAN	Q8tay0 homo sapien
59	299.5	9.6	677	2	Q28256_CANFA	Q28256 canis famil
60	298.5	9.5	649	2	Q8BGT1_MOUSE	Q8bgt1 m 12 days e
61	298.5	9.5	663	2	Q6ZPQ1_MOUSE	Q6zpq1 mus musculu
62	295.5	9.4	640	1	NGL1_MOUSE	Q8c031 mus musculu
63	295.5	9.4	640	2	Q505E5_MOUSE	Q505e5 mus musculu
64	294.5	9.4	647	2	Q50I7_BRARE	Q50i7 brachydanio
65	293.5	9.4	372	2	Q499C1_BRARE	Q499c1 brachydanio
66	293.5	9.4	809	2	Q9DBY4_MOUSE	Q9dby4 m adult mal
67	292.5	9.3	640	1	NGL1_HUMAN	Q9hcj2 homo sapien
68	292.5	9.3	811	2	Q49G2Z_RAT	Q49g2z rattus norv
69	292.5	9.3	837	2	Q80TV0_MOUSE	Q80tv0 mus musculu
70	288.5	9.2	372	2	Q7T2W3_BRARE	Q7t2w3 brachydanio
71	288.5	9.2	581	2	Q4SYI7_TETNG	Q4syi7 tetraodon n
72	288.5	9.2	640	1	Q4JIW0_HUMAN	Q4jiw0 homo sapien
73	287.5	9.2	428	2	Q4S4W6_TETNG	Q4s4w6 tetraodon n
74	287.5	9.2	713	1	LRRN5_HUMAN	Q5325 homo sapien
75	286	9.1	650	2	Q4RQ15_TETNG	Q4rq15 tetraodon n
76	285	9.1	640	2	Q4JIV9_HUMAN	Q4jlv9 homo sapien
77	284.5	9.1	457	2	Q6WZD1_BRARE	Q6wzd1 brachydanio
78	284	9.1	782	2	Q5T0V4_HUMAN	Q5t0v4 homo sapien
79	283.5	9.0	603	2	O70211_RAT	O70211 rattus norv
80	283	9.0	1515	2	Q9DE37_BRARE	Q9de37 brachydanio
81	282.5	9.0	745	2	Q6UXK2_HUMAN	Q6uxk2 homo sapien
82	282.5	9.0	785	2	Q9P263_HUMAN	Q9p263 homo sapien
83	282	9.0	626	1	GP1BA_HUMAN	P07359 homo sapien
84	281.5	9.0	603	1	ALS_RAT	P35859 rattus norv
85	281	9.0	738	2	Q90Z45_CHICK	Q90245 gallus gall
86	280	8.9	633	2	Q4SR95_TETNG	Q4sr95 tetraodon n
87	279.5	8.9	331	1	Q2YDZ4_EPTST	Q2ydz4 eptatretus
88	279.5	8.9	619	2	Q57029_MOUSE	Q57029 mus musculu
89	278.5	8.9	301	2	Q3KQP3_MOUSE	Q3kqp3 mus musculu
90	278.5	8.9	603	1	ALS_MOUSE	P70389 homo sapien
91	278.5	8.9	603	2	Q79IQ5_MOUSE	Q791q5 mus musculu
92	278.5	8.9	687	2	Q9JIL0_MOUSE	Q9jil0 mus musculu
93	278	8.9	321	2	Q6A4K4_PETMA	Q6a4k4 petromyzon
94	278	8.9	278	1	SLIT1_RAT	O88279 rattus norv
95	277	8.8	1531	2	Q4G1K9_EPTBU	Q4g1k9 eptatretus
96	277	8.8	330	2	Q316S4_BRARE	Q316s4 brachydanio
97	276.5	8.8	1532	2	Q32QN8_EPTST	Q32qn8 eptatretus
98	276	8.8	347	2	Q4RTI6_TETNG	Q4rti6 tetraodon n
99	276	8.8	1071	1	SLIT1_MOUSE	Q80tr4 mus musculu
100	276	8.8	1531	2	Q6WRI0_HUMAN	Q6wri0 mus musculu
101	275	8.7	2623	2	Q2YE01_EPTST	Q2ye01 eptatretus
102	273.5	8.7	358	2	Q6UY18_HUMAN	Q6uy18 homo sapien
103	273.5	8.7	593	1	SLIT_DROME	P24014 drosophila
104	273	8.7	1504	2	Q5RKR3_MOUSE	Q5rkr3 mus musculu

#	Accession	Organism	ID Code	N	Length	Score	Value
105	Q6zpq3	mus musculu	Q62PQ3_MOUSE	2	785	8.7	273
106	Q3s2j2	brachydanio	Q3S2J2_BRARE	2	1524	8.7	272.5
107	Q32qq2	eptatretus	Q32QQ2_EPTST	2	372	8.7	272
108	Q91xl1	mus musculu	Q91XL1_MOUSE	2	342	8.7	271.5
109	Q32q86	eptatretus	Q32QS6_EPTST	2	347	8.7	271.5
110	Q61pf0	caenorhabdi	Q61PF0_CAEBR	2	1312	8.6	271.5
111	Q32qq5	eptatretus	Q32QQ5_EPTST	2	372	8.6	271
112	Q9bzr6	homo sapien	RTN4R_HUMAN	1	473	8.6	271
113	Q9n0e3	macaca fasc	RTN4R_MACFA	1	473	8.6	271
114	Q6pk41	homo sapien	Q6PK41_HUMAN	2	541	8.6	270.5
115	Q6wzd2	brachydanio	Q6WZD2_BRARE	2	478	8.6	270
116	Q5vw18	homo sapien	Q5VW18_HUMAN	2	1461	8.6	270
117	O75093	homo sapien	SLIT1_HUMAN	2	1534	8.6	270
118	Q5vw17	homo sapien	Q5VW17_HUMAN	2	1534	8.6	270
119	Q5t0v2	petromyzon	Q5T0V2_HUMAN	2	409	8.6	268.5
120	Q6e4j7	petromyzon	Q6E4J7_PETMA	2	417	8.5	268
121	Q9de36	brachydanio	Q9DE36_BRARE	2	1512	8.5	267.5
122	Q7zxi2	xenopus lae	Q7ZXI2_XENLA	2	1529	8.5	266.5
123	Q61pl6	homo sapien	Q61PL6_HUMAN	2	460	8.5	266
124	O35930	mus musculu	O35930_MOUSE	2	734	8.5	266
125	Q5isr9	macaca fasc	Q5ISR9_MACFA	2	1044	8.5	265.5
126	Q4g1l7	eptatretus	Q4G1L7_EPTBU	2	298	8.5	265
127	Q5sx47	mus musculu	Q5SX47_MOUSE	2	734	8.5	265
128	Q13641	homo sapien	TPBG_HUMAN	1	420	8.4	264.5
129	Q2i0m4	homo sapien	Q2I0M4_HUMAN	2	334	8.4	264
130	Q5vsg2	homo sapien	Q5VSG2_HUMAN	2	334	8.4	264
131	Q4g1l1	eptatretus	Q4G1L1_EPTBU	2	352	8.4	263
132	Q2ydz5	eptatretus	Q2YDZ5_EPTST	2	308	8.4	263
133	Q5i0e1	rattus norv	Q5I0E1_RAT	2	332	8.4	263
134	Q4t0s1	tetraodon n	Q4T0S1_TETNG	2	1253	8.4	263
135	Q16wm1	aedes aegyp	Q16WM1_AEDAE	2	1393	8.4	262.5
136	Q4g1l9	eptatretus	Q4G1L9_EPTBU	2	346	8.4	262
137	P02750	homo sapien	A2GL_HUMAN	1	347	8.3	261.5
138	Q2ye28	eptatretus	Q2YE28_EPTBU	2	318	8.3	261
139	Q2ye06	eptatretus	Q2YE06_EPTST	2	341	8.3	261
140	Q88280	rattus norv	SLIT3_RAT	1	1523	8.3	260
141	Q2ye21	eptatretus	Q2YE21_EPTST	2	306	8.3	260
142	Q2ye78	eptatretus	Q2YE78_EPTST	2	370	8.3	259
143	Q6e4d1	petromyzon	Q6E4D1_PETMA	2	321	8.2	258
144	Q2ye77	eptatretus	Q2YE77_EPTST	2	370	8.2	258
145	O75094	homo sapien	SLIT3_HUMAN	1	1523	8.2	258
146	Q4s3k9	tetraodon n	Q4S3K9_TETNG	2	324	8.2	257.5
147	Q32qx0	eptatretus	Q32QX0_EPTST	2	347	8.2	257.5
148	Q4szc5	tetraodon n	Q4SZC5_TETNG	2	501	8.2	257.5
149	Q2ydz6	eptatretus	Q2YDZ6_EPTST	2	306	8.2	257
150	Q99m75	rattus norv	RTN4R_RAT	1	473	8.2	257
151	Q8bkm5	mus musculu	Q8BKM5_MOUSE	2	739	8.2	256.5
152	Q4sgg5	tetraodon n	Q4SGG5_TETNG	2	342	8.1	256
153	Q90xg4	gallus gall	Q90XG4_CHICK	2	1095	8.1	255.5
154	Q3v1m1	mus musculu	Q3V1M1_MOUSE	2	1196	8.1	254.5
155	Q8n644	homo sapien	Q8N644_HUMAN	2	528	8.1	254
156	Q9wvb4	mus musculu	SLIT3_MOUSE	1	1523	8.1	254
157	Q3uhn1	mus musculu	Q3UHN1_MOUSE	2	324	8.1	254
158	Q58s56	mus musculu	Q5SS56_MOUSE	2	347	8.1	253.5
159	Q68ck4	homo sapien	Q68CK4_HUMAN	2	429	8.1	253.5
160	Q3upm4	mus musculu	Q3UPM4_MOUSE	2	429	8.1	253.5
161	Q6gqu6	mus musculu	Q6GQU6_MOUSE	2	589	8.1	253.5
162	Q20204	caenorhabdi	Q20204_CAEEL	2	1410	8.1	253.5
163	Q32qp3	eptatretus	Q32QP3_EPTST	2	368	8.1	253
164	Q9z010	mus musculu	TPBG_MOUSE	1	426	8.1	253
165	Q3upi2	mus musculu	Q3UPI2_MOUSE	2	426	8.1	253
166	O08742	mus musculu	GPV_MOUSE	1	567	8.0	253
167	Q2ye08	eptatretus	Q2YE08_EPTST	2	323	8.0	252.5
168	Q6e4l1	petromyzon	Q6E4L1_PETMA	2	311	8.0	252
169	Q5pqv5	rattus norv	TPBG_RAT	1	426	8.0	252
170	Q3ta66	mus musculu	Q3TA66_MOUSE	2	567	8.0	252
171	Q9qzu3	mus musculu	Q9QZU3_MOUSE	2	567	8.0	252
172	Q2ydz8	eptatretus	Q2YDZ8_EPTST	2	309	8.0	251.5
173	Q99pi8	mus musculu	RTN4R_MOUSE	1	473	8.0	251
174	Q9n4g6	caenorhabdi	Q9N4G6_CAEEL	2	542	8.0	251
175	Q1ks52	pig	Q1KS52_PIG	2	606	8.0	251
176	Q7z2q7	homo sapien	Q7Z2Q7_HUMAN	2	622	8.0	251
177	Q6zwi5	homo sapien	Q62WI5_HUMAN	2	622	8.0	251
178	Q9v430	drosophila	Q9V430_DROME	2	1021	8.0	251
179	Q4rru8	tetraodon n	Q4RRU8_TETNG	2	412	8.0	250
180	Q32qq1	eptatretus	Q32QQ1_EPTST	2	347	8.0	249.5
181	Q9ulh4	homo sapien	LRFN2_HUMAN	1	789	8.0	249.5
182	Q9be71	macaca fasc	LRFN2_MACFA	1	789	7.9	249.5
183	Q6wrh9	rattus norv	Q6WRH9_RAT	1	2597	7.9	249.5
184	Q4r8y9	macaca fasc	TPBG_MACFA	1	420	7.9	248.5
185	Q2yel5	eptatretus	Q2YEI5_EPTST	2	284	7.9	248
186	Q9bzr6	homo sapien	NYX_HUMAN	1	481	7.9	248
187	Q9gzus	homo sapien	Q2MIS4_HUMAN	2	481	7.9	248
188	Q2m1s4	homo sapien	Q4GIL3_EPTBU	2	305	7.9	247.5
189	Q4gl13	eptatretus	Q32QT7_EPTST	2	323	7.9	247.5
190	Q32qt7	eptatretus	Q32QX2_EPTST	2	323	7.9	247.5
191	Q32qx2	eptatretus	Q2PNW3_XENLA	2	739	7.9	247.5
192	Q2pnw3	xenopus lae	SLIT2_MOUSE	1	1521	7.9	247.5
193	Q9rlb9	homo sapien	SLIT2_HUMAN	1	1521	7.9	247.5
194	O94813	homo sapien	Q17RU3_HUMAN	2	1529	7.9	247.5
195	Q17ru3	homo sapien	Q90WZ3_XENLA	2	1530	7.9	247.5
196	Q90wz3	xenopus lae	Q4SK16_TETNG	2	794	7.9	247
197	Q4sk16	tetraodon n	Q28WZ1_DROPS	2	1473	7.9	247
198	Q28wz1	drosophila	Q2YE14_EPTST	2	283	7.9	246.5
199	Q2ye14	eptatretus	Q2YE02_EPTST	2	323	7.9	246.5
200	Q2ye02	eptatretus	Q32QP6_EPTST	2	371	7.9	246.5
201	Q32qp6	eptatretus	Q2VGV6_PETMA	2	264	7.8	246
202	Q2vgv6	petromyzon	Q2YE10_EPTST	2	306	7.8	246
203	Q2ye10	eptatretus	Q4GIL3_EPTST	2	308	7.8	246
204	Q4gl13	eptatretus	Q2KIF2_BOVIN	2	346	7.8	246
205	Q2kif2	bos taurus	Q3UUY1_MOUSE	2	331	7.8	245.5
206	Q3uuy1	m 6 days ne	Q91W20_MOUSE	2	331	7.8	245.5
207	Q91w20	m cdna sequ	Q32QY6_EPTST	2	346	7.8	245.5
208	Q32qy6	eptatretus	Q61X58_CAEBR	2	544	7.8	245.5
209	Q61x58	caenorhabdi	Q460M5_RAT	2	788	7.8	245
210	Q460m5	rattus norv	Q4GIK6_EPTST	2	306	7.8	245
211	Q4g1k6	eptatretus	Q6E4J9_PETMA	2	321	7.8	245
212	Q6e4j9	petromyzon	LRRN3_PONPY	1	708	7.8	245
213	Q5r482	pongo pygma	Q4S6L6_TETNG	2	245	7.8	245
214	Q4s6l6	tetraodon n	O73675_XENLA	2	718	7.8	244.5
215	O73675	xenopus lae	SLIT2_RAT	1	766	7.8	244.5
216	Q9wvc1	rattus norv	LRFN2_MOUSE	1	788	7.8	244.5
217	Q80tg9	mus musculu	Q5DTL5_MOUSE	2	1593	7.8	244.5
218	Q5dtl5	mus musculu	Q32QV4_EPTST	2	346	7.8	244
219	Q32qv4	eptatretus	Q6WZD3_BRARE	1	458	7.8	244
220	Q6wzd3	brachydanio	GPV_RAT	1	567	7.8	244
221	O08770	rattus norv	LRRN3_HUMAN	1	708	7.8	244
222	Q9h3w5	homo sapien	Q32QR8_EPTST	2	347	7.8	243.5
223	Q32qr8	eptatretus	NYX_MOUSE	1	476	7.8	243.5
224	P83503	mus musculu	Q2VGX4_PETMA	2	242	7.8	243
225	Q2vgx4	petromyzon	Q2VGX3_PETMA	2	290	7.8	243
226	Q2vgx3	petromyzon	Q6E4L4_PETMA	2	321	7.8	243
227	Q6e414	petromyzon	Q32QY0_EPTST	2	323	7.7	243
228	Q32qy0	eptatretus	Q2YE75_EPTST	2	355	7.7	242.5
229	Q32qw7	eptatretus	Q32QW7_EPTST	2	371	7.7	242.5
230	Q62m54	brachydanio	Q62M54_BRARE	1	388	7.7	242.5
231	P22792	homo sapien	CPN2_HUMAN	1	545	7.7	242.5
232	Q6pck4	xenopus lae	Q6PCK4_XENLA	2	718	7.7	242.5
233	Q2vgh4	petromyzon	Q2VGH4_PETMA	2	266	7.7	242
234	Q2vgf4	petromyzon	Q2VGF4_PETMA	2	266	7.7	242
235	Q5t0v3	homo sapien	Q5T0V3_HUMAN	2	380	7.7	242
236	Q7pvz3	anopheles g	Q7PVZ3_ANOGA	2	652	7.7	242
237	Q4kp12	lampetra ap	Q4KP12_LAMAP	2	272	7.7	241.5
238	Q6e413	petromyzon	Q6E4L3_PETMA	2	311	7.7	241.5
239	Q2ydz9	eptatretus	Q2YDZ9_EPTST	2	330	7.7	241
240	Q2ydz3	eptatretus	Q2YDZ3_EPTST	2	299	7.7	240.5
241	Q32qy1	eptatretus	Q32QY1_EPTST	2	323	7.7	240.5
242	Q2ye62	eptatretus	Q2YE62_EPTST	2	323	7.7	240.5
243	Q32qx5	eptatretus	Q32QX5_EPTST	2	323	7.7	240.5
244	Q2ydz2	eptatretus	Q2YDZ2_EPTST	2	308	7.7	240
245	P40197	homo sapien	GPV_HUMAN	1	560	7.6	240
246	Q2ye04	eptatretus	Q2YE04_EPTST	2	307	7.6	239.5
247	Q8bgx3	m adult mal	Q8BGX3_MOUSE	1	370	7.6	239.5
248	Q5tu01	anopheles g	Q5TU01_ANOGA	2	786	7.6	239.5
249	Q7qct2	anopheles g	Q7QCT2_ANOGA	2	1256	7.6	238.5
250	Q2ye56	eptatretus	Q2YE56_EPTST	2	347	7.6	238.5

#					ID	Organism
251	238.5	7.6	995	2	Q29KV3_DROPS	Q29kv3 drosophila
252	238	7.6	323	2	Q4KP13_9PETR	Q4kp13 ichthyomyzo
253	238	7.6	348	2	Q2YE73_EPTST	Q2ye73 eptatretus
254	238	7.6	453	2	Q86XY1_HUMAN	Q86xy1 homo sapien
255	238	7.6	544	2	Q8UV23_9PERC	Q8uv23 sphoeroides
256	237.5	7.6	323	2	Q2YE74_EPTBU	Q2ye74 eptatretus
257	237.5	7.6	346	2	Q32R39_EPTST	Q32r39 eptatretus
258	237.5	7.6	391	2	Q9D3K0_MOUSE	Q9d3k0 m 6 days ne
259	237.5	7.6	1174	2	Q4S4C0_TETNG	Q4s4c0 tetraodon n
260	237	7.6	289	2	Q4KP06_LAMAP	Q4kp06 lampetra ap
261	237	7.6	370	2	Q8N967_HUMAN	Q8n967 homo sapien
262	237	7.6	578	1	LRC15_RAT	LRC15_RAT rattus norv
263	237	7.6	707	1	LRRN3_RAT	LRRN3_RAT rattus norv
264	237	7.6	1046	2	Q7PZJ7_ANOGA	Q7pzj7 anopheles g
265	236.5	7.5	461	2	Q4SA12_TETNG	Q4sa12 tetraodon n
266	236.5	7.5	715	2	Q4RY04_TETNG	Q4ry04 tetraodon n
267	236	7.5	306	2	Q2YDZ7_EPTST	Q2ydz7 eptatretus
268	236	7.5	707	1	LRRN3_MOUSE	LRRN3_MOUSE mus musculu
269	236	7.5	718	2	Q6PZ7_XENLA	Q6pz7 xenopus lae
270	235.5	7.5	283	2	Q2YE20_EPTST	Q2ye20 eptatretus
271	235.5	7.5	296	2	Q4G1H6_EPTST	Q4g1h6 eptatretus
272	235.5	7.5	307	2	Q2YE19_EPTST	Q2ye19 eptatretus
273	235.5	7.5	307	2	Q2YE00_EPTST	Q2ye00 eptatretus
274	235.5	7.5	579	1	LRC15_MOUSE	LRC15_MOUSE mus musculu
275	235	7.5	574	2	Q4RRR5_TETNG	Q4rrr5 tetraodon n
276	234.5	7.5	346	2	Q32R33_EPTBU	Q32r33 eptatretus
277	234.5	7.5	488	2	Q4RK86_TETNG	Q4rk86 tetraodon n
278	234.5	7.5	703	2	Q16TC8_AEDAE	Q16tc8 aedes aegyp
279	234.5	7.5	958	2	Q29LE3_DROPS	Q29le3 drosophila
280	233.5	7.5	298	2	Q6E4J4_PETMA	Q6e4j4 petromyzon
281	233.5	7.5	322	2	Q32QZ1_EPTBU	Q32qz1 eptatretus
282	233.5	7.5	346	2	Q32QY9_EPTST	Q32qy9 eptatretus
283	233.5	7.5	545	2	Q5R534_PONPY	Q5r534 pongo pygma
284	233.5	7.5	1587	2	Q17FD9_AEDAE	Q17fd9 aedes aegyp
285	233	7.4	393	2	Q32R29_EPTBU	Q32r29 eptatretus
286	233	7.4	1316	2	Q9VQ25_DROME	Q9vq25 drosophila
287	232.5	7.4	323	2	Q2YE85_EPTST	Q2ye85 eptatretus
288	232	7.4	487	2	Q4SA13_TETNG	Q4sa13 tetraodon n
289	232	7.4	766	2	Q2WF71_MOUSE	Q2wf71 mus musculu
290	231.5	7.4	283	2	Q4G1H4_EPTST	Q4g1h4 eptatretus
291	231.5	7.4	323	2	Q2YE66_EPTST	Q2ye66 eptatretus
292	231.5	7.4	323	2	Q32QS9_EPTST	Q32qs9 eptatretus
293	231.5	7.4	598	2	Q2PFR9_MACFA	Q2pfr9 macaca fasc
294	231.5	7.4	840	1	SLIK6_MOUSE	Slik6 mus musculu
295	231	7.4	294	2	Q5VT99_HUMAN	Q5vt99 homo sapien
296	231	7.4	324	2	Q32QP7_EPTST	Q32qp7 eptatretus
297	231	7.4	347	2	Q32R08_EPTBU	Q32r08 eptatretus
298	230.5	7.4	547	1	CPN2_MOUSE	Cpn2 mus musculu
299	230.5	7.4	581	2	Q49S06_HUMAN	Q49s06 homo sapien
300	230.5	7.4	619	2	Q7QBW2_ANOGA	Q7qbw2 anopheles g
301	231	7.4	766	2	Q460M4_MOUSE	Q460m4 mus musculu
302	231	7.3	787	2	Q4SW26_TETNG	Q4sw26 tetraodon n
303	230.5	7.3	257	2	Q2VGP9_PETMA	Q2vgp9 petromyzon
304	230.5	7.3	323	2	Q32QQ3_EPTST	Q32qq3 eptatretus
305	230.5	7.3	687	2	Q4SCX3_TETNG	Q4scx3 tetraodon n
306	230	7.3	332	2	Q8QFN7_ELAQU	Q8qfn7 elaphe quad
307	230	7.3	332	2	Q8QFN6_ELAQU	Q8qfn6 elaphe quad
308	230	7.3	872	2	Q4SZ04_TETNG	Q4sz04 tetraodon n
309	230	7.3	1229	2	Q4T7S0_TETNG	Q4t7s0 tetraodon n
310	229.5	7.3	233	2	Q2VGE3_PETMA	Q2vge3 petromyzon
311	229.5	7.3	323	2	Q2YE65_EPTST	Q2ye65 eptatretus
312	229.5	7.3	323	2	Q2YE70_EPTST	Q2ye70 eptatretus
313	229.5	7.3	323	2	Q32QW0_EPTST	Q32qw0 eptatretus
314	229.5	7.3	370	2	Q32R18_EPTBU	Q32r18 eptatretus
315	229.5	7.3	828	2	Q8C8T7_MOUSE	Q8c8t7 mus musculu
316	229	7.3	240	2	Q2VGN7_PETMA	Q2vgn7 petromyzon
317	229	7.3	324	2	Q32QT5_EPTST	Q32qt5 eptatretus
318	229	7.3	347	2	Q32R44_EPTBU	Q32r44 eptatretus
319	229	7.3	348	2	Q32QW2_EPTST	Q32qw2 eptatretus
320	229	7.3	581	1	LRC15_HUMAN	LRC15_HUMAN homo sapien
321	228.5	7.3	294	2	Q6E4L6_PETMA	Q6e4l6 petromyzon
322	228.5	7.3	341	1	LRC55_HUMAN	LRC55_HUMAN homo sapien
323	228.5	7.3	342	2	Q4RRU5_TETNG	Q4rru5 tetraodon n

#					ID	Organism
324	228	7.3	310	2	Q4RRQ4_TETNG	Q4rrq4 tetraodon n
325	228	7.3	322	2	Q32QP0_EPTST	Q32qp0 eptatretus
326	228	7.3	838	2	Q4SPP9_TETNG	Q4spp9 tetraodon n
327	227.5	7.3	356	1	Q8BXQ3_MOUSE	Q8bxq3 m adult ret
328	227	7.2	311	1	LRC55_MOUSE	Q4ky51 mus musculu
329	227	7.2	321	1	LRC55_RAT	Q4kli3 rattus norv
330	227	7.2	324	2	Q32R27_EPTBU	Q32r27 eptatretus
331	227	7.2	371	2	Q2YE58_EPTBU	Q2ye58 eptatretus
332	227	7.2	783	2	Q32R26_EPTBU	Q32r26 eptatretus
333	227	7.2	950	2	Q90XG2_CHICK	Q90xg2 gallus gall
334	227	7.2	227	2	Q90Z44_CHICK	Q90z44 gallus gall
335	226.5	7.2	209	2	Q2VGN5_PETMA	Q2vgn5 petromyzon
336	226.5	7.2	283	2	Q4G1I1_EPTST	Q4g1i1 eptatretus
337	226.5	7.2	298	2	Q4KP15_9PETR	Q4kp15 ichthyomyzo
338	226.5	7.2	299	2	Q4G1I9_EPTST	Q4g1i9 eptatretus
339	226.5	7.2	323	2	Q32QU1_EPTST	Q32qu1 eptatretus
340	226.5	7.2	557	1	LGI1_HUMAN	Q95970 homo sapien
341	226.5	7.2	557	1	Q1EGL2_PANTR	Q1egl2 pan troglod
342	226.5	7.2	719	1	LRFN5_HUMAN	Q96ni6 homo sapien
343	226	7.2	321	2	Q4KP16_9PETR	Q4kp16 ichthyomyzo
344	226	7.2	322	2	Q32QN1_EPTST	Q32qn1 eptatretus
345	226	7.2	364	2	Q4SQ63_TETNG	Q4sq63 tetraodon n
346	226	7.2	210	2	Q4SCF1_TETNG	Q4scf1 tetraodon n
347	225.5	7.2	257	2	Q2VGS2_PETMA	Q2vgs2 petromyzon
348	225.5	7.2	298	2	Q6E4J3_PETMA	Q6e4j3 petromyzon
349	225	7.2	733	2	Q2M032_DROPS	Q2m032 drosophila
350	225	7.2	323	2	Q32QSO_EPTST	Q32qs0 eptatretus
351	224.5	7.2	347	2	Q32QQO_EPTST	Q32qq0 eptatretus
352	224.5	7.2	218	2	Q2VGW8_PETMA	Q2vgw8 petromyzon
353	224	7.1	322	2	Q32QR2_EPTST	Q32qr2 eptatretus
354	224	7.1	1202	2	Q291L6_DROPS	Q29l16 drosophila
355	223.5	7.1	209	2	Q2VGX5_PETMA	Q2vgx5 petromyzon
356	223.5	7.1	283	2	Q4G1H8_EPTST	Q4g1h8 eptatretus
357	223.5	7.1	323	2	Q2YE55_EPTST	Q2ye55 eptatretus
358	223.5	7.1	323	2	Q32QR0_EPTST	Q32qr0 eptatretus
359	223.5	7.1	647	2	Q4SIN0_TETNG	Q4sin0 tetraodon n
360	223	7.1	289	2	Q6E4C8_PETMA	Q6e4c8 petromyzon
361	223	7.1	345	2	Q2YE83_EPTST	Q2ye83 eptatretus
362	223	7.1	349	2	Q4SH52_TETNG	Q4sh52 tetraodon n
363	222.5	7.1	323	2	Q32QW5_EPTST	Q32qw5 eptatretus
364	222.5	7.1	323	2	Q2YE67_EPTST	Q2ye67 eptatretus
365	222.5	7.1	323	2	Q32QV2_EPTST	Q32qv2 eptatretus
366	222.5	7.1	413	2	Q42I5_MOUSE	Q42i5 mus musculu
367	222.5	7.1	557	1	LGI1_RAT	Q8k4y5 rattus norv
368	222.5	7.1	557	2	Q5R945_PONPY	Q5r945 pongo pygma
369	222.5	7.1	557	2	Q5FWS7_RAT	Q5fws7 rattus norv
370	222.5	7.1	792	2	Q90Z43_CHICK	Q90z43 gallus gall
371	222	7.1	269	2	Q6E4L0_PETMA	Q6e4l0 petromyzon
372	222	7.1	348	2	Q95JJ8_MACFA	Q95jj8 macaca fasc
373	222	7.1	348	2	Q32QP2_EPTST	Q32qp2 eptatretus
374	222	7.1	222	2	Q32QN3_EPTST	Q32qn3 eptatretus
375	222	7.1	722	2	Q5PPU2_XENLA	Q5ppu2 xenopus lae
376	221.5	7.1	249	2	Q2VGK2_PETMA	Q2vgk2 petromyzon
377	221.5	7.1	323	2	Q32QV6_EPTST	Q32qv6 eptatretus
378	221.5	7.1	323	2	Q32QW6_EPTST	Q32qw6 eptatretus
379	221.5	7.1	475	2	Q4T1O9_TETNG	Q4t109 tetraodon n
380	221.5	7.1	557	1	LGI1_MOUSE	Q9ia1 mus musculu
381	221.5	7.1	719	1	LRFN5_MOUSE	Q8bxa0 mus musculu
382	221.5	7.1	721	2	Q5DTH4_MOUSE	Q5dth4 mus musculu
383	221	7.0	286	2	Q2YE07_EPTST	Q2ye07 eptatretus
384	221	7.0	322	2	Q32QS5_EPTST	Q32qs5 eptatretus
385	221	7.0	345	2	Q32QZ9_EPTST	Q32qz9 eptatretus
386	221	7.0	348	2	Q32QU7_EPTST	Q32qu7 eptatretus
387	221	7.0	1093	1	LRIG1_HUMAN	Q96ja1 homo sapien
388	221	7.0	1528	2	Q2UZU6_AEDAE	Q2uzu6 aedes aegyp
389	220.5	7.0	210	2	Q6E4M1_PETMA	Q6e4m1 petromyzon
390	220.5	7.0	306	2	Q4KP04_LAMAP	Q4kp04 lampetra ap
391	220.5	7.0	322	2	Q6E4K1_PETMA	Q6e4k1 petromyzon
392	220.5	7.0	323	2	Q32QN5_EPTST	Q32qn5 eptatretus
393	220.5	7.0	342	2	Q4RW94_TETNG	Q4rw94 tetraodon n
394	220.5	7.0	515	1	LRTM2_MOUSE	Q8bga3 mus musculu
395	220.5	7.0	515	2	Q8C8L1_HUMAN	Q8c8l1 mus musculu
396	220.5	7.0	733	2	Q24250_DROME	Q24250 drosophila

#	Score	E	Len	N	ID	Accession	Organism
397	220.5	7.0	841	1	SLIK6_HUMAN	Q9hy5y7	homo sapien
398	220	7.0	345	2	Q32R13_EPTBU	Q32r13	eptatretus
399	220	7.0	347	2	Q32R23_EPTBU	Q32r23	eptatretus
400	220	7.0	582	1	LRTM3_MOUSE	Q8bza0	mus musculu
401	220	7.0	582	1	Q8BZA0_MOUSE	Q8bza0	mus musculu
402	220	7.0	603	2	Q4SJ27_TETNG	Q4sj27	tetraodon n
403	219.5	7.0	323	2	Q32QR3_EPTST	Q32qr3	eptatretus
404	219.5	7.0	323	2	Q32QT4_EPTST	Q32qt4	eptatretus
405	219.5	7.0	323	2	Q32QW4_EPTST	Q32qw4	eptatretus
406	219.5	7.0	323	2	Q32QV3_EPTST	Q32qv3	eptatretus
407	219.5	7.0	583	2	Q4SNQ0_TETNG	Q4snq0	tetraodon n
408	219	7.0	218	2	Q2VH13_PETMA	Q2vh13	petromyzon
409	219	7.0	264	2	Q2VH48_PETMA	Q2vh48	petromyzon
410	219	7.0	324	2	Q2YE60_EPTST	Q2ye60	eptatretus
411	219	7.0	334	2	Q6P7C4_RAT	Q6p7c4	rattus norv
412	218.5	7.0	322	2	Q32R19_EPTBU	Q32r19	eptatretus
413	218.5	7.0	323	2	Q2YE76_EPTST	Q2ye76	eptatretus
414	218.5	7.0	359	2	Q6GTU0_HUMAN	Q6gtu0	homo sapien
415	218.5	7.0	618	1	LRC21_MOUSE	Q8k099	mus musculu
416	218	7.0	216	2	Q2VGH7_PETMA	Q2vgh7	petromyzon
417	218	7.0	264	2	Q2VGT2_PETMA	Q2vgt2	petromyzon
418	218	7.0	323	2	Q32R09_EPTBU	Q32r09	eptatretus
419	218	7.0	347	2	Q32R14_EPTBU	Q32r14	eptatretus
420	217.5	7.0	288	2	Q8BR15_MOUSE	Q8br15	mus musculu
421	217.5	6.9	615	2	Q4SLS7_TETNG	Q4sls7	tetraodon n
422	217.5	6.9	695	2	Q4T1Y8_TETNG	Q4t1y8	tetraodon n
423	217.5	6.9	1335	2	Q610C7_CAEBR	Q610c7	caenorhabdi
424	217	6.9	322	2	Q2YE64_EPTST	Q2ye64	eptatretus
425	217	6.9	348	2	Q32QN4_EPTST	Q32qn4	eptatretus
426	217	6.9	637	2	Q6DCV7_XENLA	Q6dcv7	xenopus lae
427	216.5	6.9	209	2	Q2VGT8_PETMA	Q2vgt8	petromyzon
428	216	6.9	263	2	Q6E4C7_PETMA	Q6e4c7	petromyzon
429	216	6.9	282	2	Q4G1I6_EPTST	Q4g1i6	eptatretus
430	216	6.9	324	2	Q32QW1_EPTST	Q32qw1	eptatretus
431	216	6.9	324	2	Q32QS4_EPTST	Q32qs4	eptatretus
432	216	6.9	514	2	Q4VBX1_MOUSE	Q4vbx1	mus musculu
433	215.5	6.9	322	2	Q32R32_EPTBU	Q32r32	eptatretus
434	215.5	6.9	322	2	Q32QT6_EPTST	Q32qt6	eptatretus
435	215.5	6.9	323	2	Q2YE61_EPTST	Q2ye61	eptatretus
436	215.5	6.9	329	2	Q56NG5_CIOIN	Q56ng5	ciona intes
437	215.5	6.9	331	1	PLIB_AGKBL	O93233	agkistrodon
438	215.5	6.9	612	2	Q4SYK9_TETNG	Q4syk9	tetraodon n
439	215	6.9	737	2	Q9VU51_DROME	Q9vu51	drosophila
440	215	6.9	322	2	Q32QX8_EPTST	Q32qx8	eptatretus
441	215	6.9	323	2	Q2YE53_EPTST	Q2ye53	eptatretus
442	214.5	6.8	323	2	Q32QY8_EPTBU	Q32qy8	eptatretus
443	214.5	6.8	347	2	Q32R00_EPTBU	Q32r00	eptatretus
444	214.5	6.8	441	1	R4RL1_HUMAN	Q32qp1	homo sapien
445	214.5	6.8	716	1	LRRN1_HUMAN	Q86un2	homo sapien
446	214.5	6.8	731	2	Q6P1M7_HUMAN	Q6uxk5	homo sapien
447	214	6.8	215	2	Q2VH33_PETMA	Q4t149	petromyzon
448	214	6.8	1535	1	Q23991_DROME	Q23991	drosophila
449	214	6.8	295	2	Q6E4C9_PETMA	Q6e4c9	petromyzon
450	214	6.8	323	2	Q32R42_EPTBU	Q32r42	eptatretus
451	214	6.8	324	2	Q2YE68_EPTST	Q2ye68	eptatretus
452	214	6.8	516	1	LRTM2_HUMAN	O43300	homo sapien
453	214	6.8	716	1	LRRN1_RAT	Q32q07	rattus norv
454	214	6.8	717	2	Q4SR34_TETNG	Q4sr34	tetraodon n
455	214	6.8	2828	1	Q9NR99_HUMAN	Q9nr99	homo sapien
456	214	6.8	238	2	Q6E4J5_PETMA	Q6e4j5	petromyzon
457	214	6.8	259	2	Q2YE23_EPTST	Q2ye23	eptatretus
458	213.5	6.8	273	2	Q4G1L2_EPTBU	Q4g1l2	eptatretus
459	213.5	6.8	323	2	Q32QW9_EPTST	Q32qw9	eptatretus
460	213.5	6.8	359	1	CHAD_HUMAN	O15335	homo sapien
461	213.5	6.8	361	1	CHAD_BOVIN	Q27972	bos taurus
470	213.5	6.8	1204	2	Q17K70_AEDAE	Q17k70	aedes aegyp
471	213	6.8	218	2	Q2VGT0_PETMA	Q2vgt0	petromyzon
472	213	6.8	322	2	Q32QX1_EPTST	Q32qx1	eptatretus
473	213	6.8	323	2	Q32QZ5_EPTBU	Q32qz5	eptatretus
474	213	6.8	347	2	Q32R04_EPTBU	Q32r04	eptatretus
475	213	6.8	716	1	LRRN1_MOUSE	Q61809	mus musculu
476	213	6.8	811	2	Q17JT2_AEDAE	Q17jt2	aedes aegyp
477	212.5	6.8	323	2	Q32QS3_EPTST	Q32qs3	eptatretus
478	212.5	6.8	604	2	Q4SHE8_TETNG	Q4she8	tetraodon n
479	212	6.8	216	2	Q2VGU4_PETMA	Q2vgu4	petromyzon
480	212	6.8	218	2	Q2VGI6_PETMA	Q2vgi6	petromyzon
481	212	6.8	276	2	Q4G1J9_EPTST	Q4g1j9	eptatretus
482	212	6.8	324	2	Q32QM9_EPTST	Q32qm9	eptatretus
483	212	6.8	445	1	R4RL1_RAT	Q80wd0	rattus norv
484	212	6.7	918	2	O7Q3F0_ANOGA	O7q3f0	anopheles g
485	211.5	6.7	192	2	Q6E4I9_PETMA	Q6e4i9	petromyzon
486	211.5	6.7	270	2	Q6E4L7_EPTST	Q6e4l7	eptatretus
487	211.5	6.7	322	2	Q32R35_EPTBU	Q32r35	eptatretus
488	211.5	6.7	323	2	Q2YE72_EPTST	Q2ye72	eptatretus
489	211.5	6.7	323	2	Q32QU9_EPTST	Q32qu9	petromyzon
490	211.5	6.7	323	2	Q32QS7_EPTST	Q32qs7	petromyzon
491	211.5	6.7	518	2	Q5R712_PONPY	Q5r712	pongo pygma
492	211	6.7	876	2	Q16L90_AEDAE	Q16l90	aedes aegyp
493	211	6.7	187	2	Q6E4I2_PETMA	Q6e4i2	petromyzon
494	211	6.7	218	2	Q2VGR7_PETMA	Q2vgr7	petromyzon
495	211	6.7	581	1	LRTM3_HUMAN	Q86vh5	homo sapien
496	211	6.7	581	1	LRTM3_MACFA	Q9bgp6	macaca fasc
497	211	6.7	581	2	Q2NKX7_HUMAN	Q2nkx7	homo sapien
498	210.5	6.7	209	2	Q2VGR9_PETMA	Q2vgr9	petromyzon
499	210.5	6.7	257	2	Q4G1M3_EPTBU	Q4g1m3	petromyzon
500	210.5	6.7	321	2	Q6E4L5_PETMA	Q6e4l5	petromyzon
501	210.5	6.7	322	2	Q32R37_EPTBU	Q32r37	eptatretus
502	210.5	6.7	322	2	Q32R10_EPTBU	Q32r10	eptatretus
503	210.5	6.7	4303	1	PKD1_HUMAN	P98161	homo sapien
504	210	6.7	264	2	Q2VGI2_PETMA	Q2vgi2	petromyzon
505	210	6.7	324	2	Q2YE50_EPTST	Q2ye50	petromyzon
506	210	6.7	324	2	Q32QU4_EPTST	Q32qu4	eptatretus
507	210	6.7	324	2	Q32QT0_EPTST	Q32qt0	eptatretus
508	210	6.7	324	2	Q32QS2_EPTST	Q32qs2	eptatretus
509	210	6.7	358	1	CHAD_RAT	O70210	rattus norv
510	210	6.7	1028	1	Q865R7_PIG	Q865r7	sus scrofa
511	209.5	6.7	214	2	Q6E4H0_PETMA	Q6e4h0	petromyzon
512	209.5	6.7	322	2	Q32R06_EPTBU	Q32r06	eptatretus
513	209.5	6.7	322	2	Q32R12_EPTBU	Q32r12	eptatretus
514	209.5	6.7	323	2	Q32QQ8_EPTST	Q32qq8	eptatretus
515	209.5	6.7	323	2	Q32QS1_EPTST	Q32qs1	eptatretus
516	209.5	6.7	382	2	Q32QU6_EPTST	Q32qu6	eptatretus
517	209.5	6.7	382	1	Q1EGK9_PANTR	Q1egk9	pan troglod
518	209	6.7	533	2	Q5E9T6_BOVIN	Q5e9t6	bos taurus
519	209	6.7	211	2	Q6E4I3_PETMA	Q6e4i3	petromyzon
520	209	6.7	216	2	Q2VGQ6_PETMA	Q2vgq6	petromyzon
521	209	6.7	257	2	Q6E4J6_PETMA	Q6e4j6	petromyzon
522	209	6.7	322	2	Q32QW8_EPTBU	Q32qw8	eptatretus
523	209	6.7	323	2	Q32R01_EPTBU	Q32r01	eptatretus
524	209	6.7	358	1	CHAD_MOUSE	O55226	mus musculu
525	209.5	6.7	391	2	Q5SUV4_MOUSE	Q5suv4	mus musculu
526	209	6.7	391	2	Q458B7_TETNG	Q458b7	tetraodon n
527	209	6.7	1091	1	LRIG1_MOUSE	P70193	mus musculu
528	208.5	6.7	1262	2	Q29L45_DROPS	Q29145	drosophila
529	208.5	6.7	350	2	Q5RH06_BRARE	Q5rh06	brachydanio
530	208.5	6.6	382	1	PRELP_HUMAN	P51888	homo sapien
531	208.5	6.6	382	2	Q6FHG6_HUMAN	Q6fhg6	homo sapien
532	208.5	6.6	382	2	Q6FG38_HUMAN	Q6fg38	homo sapien
533	208.5	6.6	445	1	R4RL1_MOUSE	Q8k085	mus musculu
534	208.5	6.6	479	2	Q6X3Y5_BRARE	Q6x3y5	brachydanio
535	208.5	6.6	518	1	LRTM4_HUMAN	Q86vh4	homo sapien
536	208.5	6.6	518	2	Q4FZ98_HUMAN	Q4fz98	homo sapien
537	208.5	6.6	519	1	Q4KMX1_HUMAN	Q4kmx1	homo sapien
538	208.5	6.6	537	1	LGI4_HUMAN	Q8n135	homo sapien
539	208.5	6.6	590	2	Q6UXJ7_HUMAN	Q6uxj7	homo sapien
540	208	6.6	218	2	Q2VGF5_PETMA	Q2vgf5	petromyzon
541	208	6.6	322	2	Q2YE51_EPTST	Q2ye51	eptatretus
542	208	6.6	649	2	Q9VK22_DROME	Q9vk22	drosophila

Rank	Score	pI	Score	ID	Length	Flag	Accession	Species
543	207.5	6.6	207.5	Q6E4F0_PETMA	180	2	Q6e4f0	petromyzon
544	207.5	6.6	207.5	Q32QT2_EPTST	323	2	Q32qt2	eptatretus
545	207.5	6.6	207.5	Q4S074_TETNG	330	2	Q4s074	tetraodon n
546	207.5	6.6	207.5	Q6ZT31_HUMAN	518	2	Q6zt31	homo sapien
547	207.5	6.6	207.5	Q17GD4_AEDAE	610	2	Q17gd4	aedes aegyp
548	207	6.6	207	GP124_MOUSE	1329	1	Q91zv8	mus musculu
549	207	6.6	207	LRC52_HUMAN	313	1	Q8n7c0	homo sapien
550	207	6.6	207	Q2YE80_EPTBU	323	2	Q2ye80	eptatretus
551	207	6.6	207	Q32R43_EPTBU	323	2	Q32r43	eptatretus
552	207	6.6	207	Q6P0D2_BRARE	536	2	Q6p0d2	brachydanio
553	207	6.6	207	Q2HPG2_BRARE	537	2	Q2hpg2	brachydanio
554	207	6.6	207	Q50L44_CHICK	613	2	Q50l44	gallus gall
555	207	6.6	207	CT075_HUMAN	740	1	Q8wut4	homo sapien
556	207	6.6	207	O08852_MOUSE	4293	2	O08852	mus musculu
557	206.5	6.6	206.5	Q2VGE9_PETMA	192	2	Q2vge9	petromyzon
558	206.5	6.6	206.5	Q6E4K6_PETMA	270	2	Q6e4k6	petromyzon
559	206.5	6.6	206.5	Q6E4C1_PETMA	274	2	Q6e4c1	petromyzon
560	206.5	6.6	206.5	Q6E4B9_PETMA	274	2	Q6e4b9	petromyzon
561	206.5	6.6	206.5	Q6E4L2_PETMA	294	2	Q6e4l2	petromyzon
562	206.5	6.6	206.5	Q32QU8_EPTST	323	2	Q32qu8	eptatretus
563	206.5	6.6	206.5	Q5U4S7_XENLA	327	2	Q5u4s7	xenopus lae
564	206.5	6.6	206.5	Q9D1T0_MOUSE	614	2	Q9d1t0	mus musculu
565	206	6.6	206	Q2VGU6_PETMA	218	2	Q2vgu6	petromyzon
566	206	6.6	206	Q32QX7_EPTST	324	2	Q32qx7	eptatretus
567	206	6.6	206	TSK_HUMAN	353	1	Q9bz20	homo sapien
568	206	6.6	206	PRELP_BOVIN	381	1	Q9gkn8	bos taurus
569	206	6.6	206	O14498_HUMAN	428	2	O14498	homo sapien
570	206	6.6	206	Q5TPW2_ANOGA	539	2	Q5tpw2	anopheles g
571	206	6.6	206	Q3URE9_MOUSE	606	2	Q3ure9	mus musculu
572	206	6.6	206	Q8BLC0_MOUSE	606	2	Q8blc0	m adult mal
573	206	6.6	206	Q8BZD4_MOUSE	606	2	Q8bzd4	mus musculu
574	206	6.6	206	Q5U1A7_DROME	738	2	Q5u1a7	drosophila
575	206	6.6	206	LRIG2_MOUSE	1054	1	Q52kr2	mus musculu
576	206	6.6	206	Q4TAT9_TETNG	1127	2	Q4tat9	tetraodon n
577	205.5	6.6	205.5	Q6E4H2_PETMA	212	2	Q6e4h2	petromyzon
578	205.5	6.6	205.5	Q6DH76_BRARE	479	2	Q6dh76	brachydanio
579	205.5	6.6	205.5	Q99KT6_MOUSE	492	2	Q99kt6	mus musculu
580	205.5	6.6	205.5	LRTM4_MOUSE	590	1	Q80xg9	mus musculu
581	205	6.5	205	Q4G1K4_EPTST	248	2	Q4g1k4	eptatretus
582	205	6.5	205	Q4G1L6_EPTBU	256	2	Q4g1l6	eptatretus
583	205	6.5	205	Q32QR9_EPTST	320	2	Q32qr9	eptatretus
584	205	6.5	205	Q2YE54_EPTST	322	2	Q2ye54	eptatretus
585	205	6.5	205	Q2YE63_EPTST	322	2	Q2ye63	eptatretus
586	205	6.5	205	Q32QN6_EPTST	324	2	Q32qn6	eptatretus
587	205	6.5	205	Q2YE84_EPTST	324	2	Q2ye84	eptatretus
588	205	6.5	205	Q4RU74_TETNG	486	2	Q4ru74	tetraodon n
589	205	6.5	205	Q5RDJ4_PONPY	614	2	Q5rdj4	pongo pygma
590	205	6.5	205	Q9N008_MACFA	614	2	Q9n008	macaca fasc
591	205	6.5	205	Q96FES_HUMAN	620	2	Q96fes	homo sapien
592	204.5	6.5	204.5	Q32R05_EPTST	322	2	Q32r03	eptatretus
593	204.5	6.5	204.5	Q32QY2_EPTST	323	2	Q32qy2	eptatretus
594	204.5	6.5	204.5	Q8C1V9_MOUSE	463	2	Q8c1v9	mus musculu
595	204	6.5	204	Q2VGM5_PETMA	196	2	Q2vgm5	petromyzon
596	204	6.5	204	Q2YE25_EPTST	276	2	Q2ye25	eptatretus
597	204	6.5	204	Q32R20_EPTBU	323	2	Q32r20	eptatretus
598	204	6.5	204	Q2YE81_EPTBU	323	2	Q2ye81	eptatretus
599	204	6.5	204	TSK_RAT	353	1	Q6qmy6	rattus norv
600	204	6.5	204	Q9V7J8_DROME	1173	2	Q9v7j8	drosophila
601	204	6.5	204	Q2VGZ2_PETMA	1306	2	Q2vgz2	petromyzon
602	204	6.5	204	Q32QX3_EPTST	219	2	Q32qx3	eptatretus
603	203.5	6.5	203.5	Q6AI13_HUMAN	845	2	Q6ai13	homo sapien
604	203.5	6.5	203.5	Q9VKG1_DROME	894	2	Q9vkg1	drosophila
605	203.5	6.5	203.5	Q53ME4_ORYSA	1061	2	Q53me4	oryza sativ
606	203.5	6.5	203.5	LRIG2_HUMAN	1065	1	Q94898	homo sapien
607	203.5	6.5	203.5	Q2VGC8_PETMA	218	2	Q2vgc8	petromyzon
608	203	6.5	203	Q6E4B6_PETMA	269	2	Q6e4b6	petromyzon
609	203	6.5	203	Q2YE17_EPTST	286	2	Q2ye17	eptatretus
610	203	6.5	203	Q32Q24_EPTBU	321	2	Q32q24	eptatretus
611	203	6.5	203	Q32R15_EPTBU	323	2	Q32r15	eptatretus
612	203	6.5	203	Q32QR5_EPTST	324	2	Q32qr5	eptatretus
613	203	6.5	203	Q2YE71_EPTST	324	2	Q2ye71	eptatretus
614	203	6.5	203	Q5NVQ6_PONPY	428	2	Q5nvq6	pongo pygma
616	203	6.5	203	LRC40_MACFA	602	1	Q4rjp6	macaca fasc
617	203	6.5	203	Q4SLZ4_TETNG	703	2	Q4slz4	tetraodon n
618	203	6.5	203	Q9NBK9_DROME	1514	2	Q9nbk9	drosophila
619	203	6.5	203	Q6NN49_DROME	1514	2	Q6nn49	drosophila
620	203	6.5	203	Q9VUN0_DROME	1514	2	Q9vun0	drosophila
621	202.5	6.5	202.5	Q2VGR8_PETMA	197	2	Q2vgr8	petromyzon
622	202.5	6.5	202.5	Q2VGV9_PETMA	209	2	Q2vgv9	petromyzon
623	202.5	6.5	202.5	Q4G1H5_EPTST	259	2	Q4g1h5	eptatretus
624	202.5	6.5	202.5	Q4G1K1_EPTST	259	2	Q4g1k1	eptatretus
625	202.5	6.5	202.5	Q6E4J2_PETMA	274	2	Q6e4j2	petromyzon
626	202.5	6.5	202.5	Q32QZ8_EPTBU	322	2	Q32qz8	eptatretus
627	202.5	6.5	202.5	Q4RIG0_TETNG	829	2	Q4rig0	tetraodon n
628	202	6.4	202	Q4KPL1_LAMAP	271	2	Q4kpl1	lampetra ap
629	202	6.4	202	Q2YE57_EPTST	300	2	Q2ye57	eptatretus
630	202	6.4	202	Q32R36_EPTST	321	2	Q32r36	eptatretus
631	202	6.4	202	Q32R38_EPTBU	321	2	Q32r38	eptatretus
632	202	6.4	202	Q32QS8_EPTST	324	2	Q32qs8	eptatretus
633	202	6.4	202	Q5VQM7_ORYSA	1117	2	Q5vqm7	oryza sativ
634	202	6.4	202	Q2M1B4_DROPS	1501	2	Q2m1b4	drosophila
635	201.5	6.4	201.5	Q6E4D7_PETMA	187	2	Q6e4d7	petromyzon
636	201.5	6.4	201.5	Q4G1J5_EPTST	275	2	Q4g1j5	eptatretus
637	201.5	6.4	201.5	Q96OD1_DROME	457	2	Q96od1	drosophila
638	201.5	6.4	201.5	Q4RG59_TETNG	524	2	Q4rg59	tetraodon n
639	201.5	6.4	201.5	Q4RF95_TETNG	551	2	Q4rf95	tetraodon n
640	201.5	6.4	201.5	Q8BZ20_HUMAN	606	2	Q9bz20	homo sapien
641	201.5	6.4	201.5	P91644_DROME	892	2	P91644	drosophila
642	201.5	6.4	201.5	Q9VZZ4_DROME	1527	2	Q9vzz4	drosophila
643	201	6.4	201	Q6E4H6_PETMA	213	2	Q6e4h6	petromyzon
644	201	6.4	201	Q6E4K9_PETMA	218	2	Q6e4k9	petromyzon
645	201	6.4	201	Q32QT1_EPTST	322	2	Q32qt1	eptatretus
646	201	6.4	201	Q4S8M5_TETNG	336	2	Q4s8m5	tetraodon n
647	201	6.4	201	TSK_MOUSE	354	1	Q8cbr6	mus musculu
648	201	6.4	201	LRC40_HUMAN	602	1	Q9h1a6	homo sapien
649	201	6.4	201	Q5BL20_BRARE	712	2	Q5bl20	brachydanio
650	200.5	6.4	200.5	Q29C89_DROPS	1391	2	Q29c89	drosophila
651	200.5	6.4	200.5	Q29MX7_DROPS	815	2	Q29mx7	drosophila
652	200.5	6.4	200.5	SLIK2_HUMAN	845	1	Q9h156	homo sapien
653	200.5	6.4	200.5	Q2KHN3_HUMAN	1336	2	Q2khn3	homo sapien
654	200.5	6.4	200.5	Q2XXV6_DROYA	1337	2	Q2xxv6	drosophila
655	200.5	6.4	200.5	Q2XXV7_DROYA	218	2	Q2xxv7	drosophila
656	200	6.4	200	Q2VGY1_PETMA	280	2	Q2vgy1	petromyzon
657	200	6.4	200	Q2YE26_EPTBU	460	2	Q2ye26	eptatretus
658	200	6.4	200	Q4RK03_TETNG	547	2	Q4rk03	tetraodon n
659	200	6.4	200	Q1EGK1_FUGRU	616	2	Q1egk1	fugu rubrip
660	200	6.4	200	Q58A95_CAEEL	653	2	Q58a95	caenorhabdi
661	200	6.4	200	O02329_CAEEL	227	2	O02329	caenorhabdi
662	199.5	6.4	199.5	Q4SP28_TETNG	261	2	Q4sp28	tetraodon n
663	199.5	6.4	199.5	Q4GLL4_EPTBU	319	2	Q4gll4	eptatretus
664	199.5	6.4	199.5	Q32QN9_EPTST	622	2	Q32qn9	eptatretus
665	199.5	6.3	199.5	Q66HV9_BRARE	260	2	Q66hv9	brachydanio
666	199	6.3	199	Q2YE05_EPTST	298	2	Q2ye05	eptatretus
667	199	6.3	199	Q32QW3_EPTST	322	2	Q32qw3	eptatretus
668	199	6.3	199	Q32QV5_EPTST	322	2	Q32qv5	eptatretus
669	199	6.3	199	Q32QV8_EPTST	323	2	Q32qv8	eptatretus
670	199	6.3	199	Q32R07_EPTST	323	2	Q32r07	eptatretus
671	199	6.3	199	Q32QY5_EPTST	323	2	Q32qy5	eptatretus
672	199	6.3	199	Q32R24_EPTBU	324	2	Q32r24	eptatretus
673	199	6.3	199	Q32QT9_EPTST	324	2	Q32qt9	eptatretus
674	199	6.3	199	SLIK2_MOUSE	846	1	Q810c0	mus musculu
675	199	6.3	199	Q4ST3_CABEL	862	2	Q4st3	caenorhabdi
676	199	6.3	199	Q21043_CABEL	1328	2	Q21043	caenorhabdi
677	198.5	6.3	198.5	Q4G1J4_EPTST	259	2	Q4g1j4	eptatretus
678	198.5	6.3	198.5	Q6YN44_HUMAN	320	2	Q6yn44	homo sapien
679	198.5	6.3	198.5	Q32R17_EPTBU	322	2	Q32r17	eptatretus
680	198.5	6.3	198.5	Q1EGL0_PANTR	548	2	Q1eglo	pan troglo
681	198.5	6.3	198.5	LRC21_RAT	617	1	Q9mh2	rattus norv
682	198.5	6.3	198.5	Q4SWG9_TETNG	741	2	Q4swg9	tetraodon n
683	198.5	6.3	198.5	Q7XR24_ORYSA	873	2	Q7xr24	oryza sativ
684	198.5	6.3	198.5	GP124_HUMAN	1331	1	Q96pel	homo sapien
685	198	6.3	198	Q2VH08_PETMA	192	2	Q2vh08	petromyzon
686	198	6.3	198	Q32QN7_EPTST	298	2	Q32qn7	eptatretus
687	198	6.3	198	Q32QP4_EPTST	322	2	Q32qp4	eptatretus
688	198	6.3	198	Q32R16_EPTBU	323	2	Q32r16	eptatretus

#	E	Bits	ID	N	Len	Species
689	6.3	198	Q32R22_EPTBU	2	323	eptatretus
690	6.3	198	Q32QP8_EPTST	2	324	eptatretus
691	6.3	198	Q7SYE5_BRARE	2	363	brachydanio
692	6.3	198	LRC40_PONPY	1	602	pongo pygma
693	6.3	197.5	Q2VGP6_PETMA	2	193	petromyzon
694	6.3	197.5	Q6E4K3_PETMA	2	280	petromyzon
695	6.3	197.5	Q6E4K8_PETMA	2	300	petromyzon
696	6.3	197.5	Q32QU3_EPTST	2	323	eptatretus
697	6.3	197.5	Q4VBZ3_HUMAN	2	441	homo sapien
698	6.3	197.5	Q9VE49_DROME	2	537	drosophila
699	6.3	197.5	LGI3_HUMAN	1	548	homo sapien
700	6.3	197.5	Q4R4H3_MACFA	2	548	macaca fasc
701	6.3	197.5	Q4SIX2_TETNG	2	818	tetraodon n
702	6.3	197.5	Q4SFB0_TETNG	2	835	tetraodon n
703	6.3	197.5	GP125_HUMAN	1	1321	homo sapien
704	6.3	197	Q2YE16_EPTST	2	248	eptatretus
705	6.3	197	Q32QQ9_EPTST	2	320	eptatretus
706	6.3	197	Q32QQ6_EPTST	2	322	eptatretus
707	6.3	197	Q9HBL6_HUMAN	2	345	homo sapien
708	6.3	197	Q6YXX5_ORYSA	2	694	oryza sativ
709	6.3	197	Q5XWD3_HUMAN	2	1093	homo sapien
710	6.3	196.5	Q2VGH6_PETMA	2	209	petromyzon
711	6.3	196.5	Q4G1J3_EPTST	2	259	eptatretus
712	6.3	196.5	Q2YE12_EPTST	2	259	eptatretus
713	6.3	196.5	Q4G1J1_EPTST	2	261	eptatretus
714	6.3	196.5	Q32QY4_EPTBU	2	322	eptatretus
715	6.3	196.5	Q2LZ92_DROPS	2	551	drosophila
716	6.3	196.5	Q2XXV5_DROER	2	1332	drosophila
717	6.3	196	Q2XXW0_DROME	2	1333	drosophila
718	6.3	196	Q6E4D0_PETMA	2	263	petromyzon
719	6.3	196	Q32QX6_EPTST	2	300	eptatretus
720	6.3	196	Q15142_HUMAN	2	3638	homo sapien
721	6.2	195.5	Q1EGJ6_CHICK	2	274	gallus gall
722	6.2	195.5	Q32QZ6_EPTBU	2	298	eptatretus
723	6.2	195.5	Q2YE59_EPTST	2	323	eptatretus
724	6.2	195.5	Q58DI7_BOVIN	2	370	bos taurus
725	6.2	195	PRELP_MOUSE	1	378	mus musculu
726	6.2	195	Q54380_MOUSE	2	378	mus musculu
727	6.2	195	Q29KW0_DROPS	2	543	drosophila
728	6.2	195	Q86PM1_DROME	2	917	drosophila
729	6.2	195	Q9VWI6_DROME	2	931	drosophila
730	6.2	195	Q32QP9_EPTST	2	322	eptatretus
731	6.2	195	Q4R5H2_MACFA	2	440	macaca fasc
732	6.2	195	Q1EGJ8_CHICK	2	526	gallus gall
733	6.2	195	Q6NUK3_HUMAN	2	614	homo sapien
734	6.2	195	Q6UXM3_HUMAN	2	620	homo sapien
735	6.2	195	SLIK4_HUMAN	1	837	homo sapien
736	6.2	195	Q5JXG3_HUMAN	2	1536	homo sapien
737	6.2	195	Q29DD0_DROPS	2	322	drosophila
738	6.2	194.5	Q2YE82_EPTBU	2	323	eptatretus
739	6.2	194.5	Q32QV9_EPTST	2	369	eptatretus
740	6.2	194.5	TSK_CHICK	1	680	gallus gall
741	6.2	194.5	Q3MHH9_BOVIN	2	693	bos taurus
742	6.2	194.5	Q7Z3D0_HUMAN	2	699	homo sapien
743	6.2	194.5	ECM2_HUMAN	1	699	homo sapien
744	6.2	194.5	Q5T9F2_HUMAN	2	737	homo sapien
745	6.2	194.5	Q965M3_CAEEL	2	881	caenorhabdi
746	6.2	194.5	Q965M2_CAEEL	2	1630	caenorhabdi
747	6.2	194.5	LAP4_HUMAN	1	192	homo sapien
748	6.2	194	Q2VGJ7_PETMA	2	258	petromyzon
749	6.2	194	Q4G1J0_EPTST	2	258	eptatretus
750	6.2	194	Q4G1I0_EPTST	2	263	eptatretus
751	6.2	194	Q6E4C0_PETMA	2	320	petromyzon
752	6.2	194	Q32QT3_EPTST	2	611	eptatretus
753	6.2	194	Q4RHK3_TETNG	2	692	tetraodon n
754	6.2	194	Q4RV46_TETNG	2	836	tetraodon n
755	6.2	194	Q9V9V6_DROME	2	186	drosophila
756	6.2	193.5	Q6E4H8_PETMA	2	270	petromyzon
757	6.2	193.5	Q4KP03_LAMAP	2	273	lampetra ap
758	6.2	193.5	Q4G1M1_EPTBU	2	377	eptatretus
759	6.2	193.5	PRELP_RAT	1	378	rattus norv
760	6.2	193.5	Q8CAZ5_MOUSE	2	377	mus musculu
761	6.2	193.5	Q61DG7_DROME	2	433	drosophila

#	Bits	E	Len	N	ID	Accession	Species
762	193.5	6.2	545	1	LGI2_HUMAN	Q8n0v4	homo sapien
763	193.5	6.2	545	2	Q3MIN2_HUMAN	Q3min2	homo sapien
764	193.5	6.2	545	2	Q1EGL1_PANTR	Q1egl1	pan troglod
765	193.5	6.2	574	2	Q60W68_CAEBR	Q60w68	caenorhabdi
766	193.5	6.2	721	1	Y2082_MYCTU	Q10690	mycobacteri
767	193.5	6.2	721	2	Q7TZ24_MYCBO	Q7tz24	mycobacteri
768	193.5	6.2	816	2	Q1KL20_FUGRU	Q1kl20	fugu rubrip
769	193.5	6.2	863	2	Q46A62_METBF	Q46a62	methanosarc
770	193.5	6.2	881	2	Q2XY26_DROME	Q2xy26	drosophila
771	193.5	6.2	881	2	Q2XY24_DROSI	Q2xy24	drosophila
772	193.5	6.2	910	1	PIDD_HUMAN	Q9hb75	homo sapien
773	193.5	6.2	967	2	Q3UVD5_MOUSE	Q3uvd5	mus musculu
774	193.5	6.2	977	1	SLIK3_HUMAN	O94933	homo sapien
775	193.5	6.2	977	2	Q1RMY6_HUMAN	Q1rmy6	homo sapien
776	193.5	6.2	1333	2	Q2XXV8_DROSI	Q2xxv8	drosophila
777	193.5	6.2	1333	2	Q2XXV9_DROSI	Q2xxv9	drosophila
778	193	6.2	252	2	Q4G1I2_EPTST	Q4g1i2	eptatretus
779	193	6.2	319	2	Q32R40_EPTBU	Q32r40	eptatretus
780	193	6.2	321	2	Q32R11_EPTBU	Q32r11	eptatretus
781	193	6.2	324	2	Q32QN2_EPTST	Q32qn2	eptatretus
782	193	6.2	497	2	Q4SZU8_TETNG	Q4szu8	tetraodon n
783	193	6.2	538	2	Q2LZK6_DROPS	Q2lzk6	drosophila
784	193	6.2	545	2	Q2HPF8_BRARE	Q2hpf8	brachydanio
785	193	6.2	550	2	Q9VJN8_DROME	Q9vjn8	drosophila
786	193	6.2	743	2	Q17AC3_AEDAE	Q17ac3	aedes aegyp
787	192.5	6.1	185	2	Q2VGZ4_PETMA	Q2vgz4	petromyzon
788	192.5	6.1	187	2	Q6E4D5_PETMA	Q6e4d5	petromyzon
789	192.5	6.1	195	2	Q2VH18_PETMA	Q2vh18	petromyzon
790	192.5	6.1	214	2	Q6E4G0_PETMA	Q6e4g0	petromyzon
791	192.5	6.1	259	2	Q4G1H7_EPTST	Q4g1h7	eptatretus
792	192.5	6.1	270	2	Q6E4K0_PETMA	Q6e4k0	petromyzon
793	192.5	6.1	299	2	Q32QV1_EPTST	Q32qv1	eptatretus
794	192.5	6.1	322	2	Q32QY3_EPTBU	Q32qy3	eptatretus
795	192.5	6.1	428	2	Q6GU68_MOUSE	Q6gu68	mus musculu
796	192.5	6.1	542	2	Q50DZ7_MOUSE	Q50dz7	mus musculu
797	192.5	6.1	575	2	Q23580_CAEEL	Q23580	caenorhabdi
798	192.5	6.1	887	2	Q2XY21_DROER	Q2xy21	drosophila
799	192.5	6.1	1093	2	Q6HA06_CRAGI	Q6ha06	crassostrea
800	192	6.1	265	2	Q6E4K2_PETMA	Q6e4k2	petromyzon
801	192	6.1	273	2	Q6E4C5_PETMA	Q6e4c5	petromyzon
802	192	6.1	300	2	Q2YE86_EPTST	Q2ye86	eptatretus
803	192	6.1	548	1	LGI3_MOUSE	Lgi3	mus musculu
804	192	6.1	548	2	Q3V1R3_MOUSE	Q3v1r3	mus musculu
805	192	6.1	627	2	Q6DN14_LEICH	Q6dn14	leishmania
806	191.5	6.1	185	2	Q2VGS8_PETMA	Q2vgs8	petromyzon
807	191.5	6.1	187	2	Q6E4I7_PETMA	Q6e4i7	petromyzon
808	191.5	6.1	193	2	Q2VGY8_PETMA	Q2vgy8	petromyzon
809	191.5	6.1	204	2	Q6E4J8_PETMA	Q6e4j8	petromyzon
810	191.5	6.1	915	1	PIDD_MOUSE	Q9erv7	mus musculu
811	191.5	6.1	980	1	SLIK3_MOUSE	Q810b9	mus musculu
812	191.5	6.1	980	2	Q6NZM5_MOUSE	Q6nzm5	mus musculu
813	191	6.1	192	2	Q2VGN8_PETMA	Q2vgn8	petromyzon
814	191	6.1	194	2	Q2VGE8_PETMA	Q2vge8	petromyzon
815	191	6.1	271	2	Q4KP00_LAMAP	Q4kp00	lampetra ap
816	191	6.1	440	2	Q5RCQ8_PONPY	Q5rcq8	pongo pygma
817	191	6.1	456	2	Q28XA4_DROPS	Q28xa4	drosophila
818	191	6.1	536	2	Q173K1_AEDAE	Q173k1	aedes aegyp
819	191	6.1	610	2	Q4T1M0_TETNG	Q4t1m0	tetraodon n
820	191	6.1	757	2	Q28XQ2_DROPS	Q28xq2	drosophila
821	191	6.1	868	2	Q2XQ10_CHICK	Q2xq10	gallus gall
822	190.5	6.1	251	2	Q4G1I7_EPTST	Q4g1i7	eptatretus
823	190.5	6.1	536	2	Q2HPG1_BRARE	Q2hpg1	brachydanio
824	190.5	6.1	894	2	Q5H721_FUGRU	Q5h721	fugu rubrip
825	190.5	6.1	1238	2	Q6NR19_DROME	Q6nr19	drosophila
826	190.5	6.1	1343	2	Q17NJ1_AEDAE	Q17nj1	aedes aegyp
827	190.5	6.1	1535	2	Q9VPF0_DROME	Q9vpf0	drosophila
828	190	6.1	191	2	Q6E4H3_PETMA	Q6e4h3	petromyzon
829	190	6.1	536	2	Q16P99_AEDAE	Q16p99	aedes aegyp
830	190	6.1	639	2	Q4RE68_TETNG	Q4re68	tetraodon n
831	190	6.1	654	2	Q628N6_CAEBR	Q628n6	caenorhabdi
832	190	6.1	733	1	CT075_MOUSE	P59983	mus musculu
833	190	6.1	1119	1	LRIG3_HUMAN	Q6uxm1	homo sapien
834	190	6.1	1346	2	Q9V477_DROME	Q9v477	drosophila

Row	Accession	Description	ID	N	Length	pI	Score
835	Q6xhb1	dictyosteli	Q6XHB1_DICDI	2	2800	6.1	190
836	Q1zxd6	dictyosteli	Q1ZXD6_DICDI	2	2800	6.1	190
837	Q4g1j7	eptatretus	Q4G1J7_EPTST	2	252	6.0	189.5
838	Q4rsx9	tetraodon n	Q4RSX9_TETNG	2	370	6.0	189.5
839	Q2xy23	drosophila	Q2XY23_DROYA	2	880	6.0	189.5
840	Q2vgp2	petromyzon	Q2VGP2_PETMA	2	192	6.0	189
841	Q32qu2	eptatretus	Q32QU2_EPTST	2	298	6.0	189
842	P28653	mus musculu	PGS1_MOUSE	1	369	6.0	189
843	P47853	rattus norv	PGS1_RAT	1	369	6.0	189
844	Q3tny9	m 15 days e	Q3TNY9_MOUSE	2	369	6.0	189
845	Q4t5r5	tetraodon n	Q4T5R5_TETNG	2	627	6.0	189
846	Q4qgi8	leishmania	Q4QGI8_LEIMA	2	760	6.0	189
847	Q9sn46	arabidopsis	Q9SN46_ARATH	2	839	6.0	189
848	Q9vad1	drosophila	Q9VAD1_DROME	2	1392	6.0	189
849	Q7yqk5	canis famil	Q7YQK5_CANFA	2	4311	6.0	189
850	Q32qv7	eptatretus	Q32QV7_EPTST	2	348	6.0	188.5
851	Q6gmi5	brachydanio	Q6GMI5_BRARE	2	369	6.0	188.5
852	Q1lxa7	brachydanio	Q1LXA7_BRARE	2	370	6.0	188.5
853	Q504e0	brachydanio	Q504E0_BRARE	2	370	6.0	188.5
854	Q9ddz7	petromyzon	Q9DDZ7_PETMA	2	410	6.0	188.5
855	Q5syh5	mus musculu	Q5SYH5_MOUSE	2	433	6.0	188.5
856	Q63912	mus musculu	OMGP_MOUSE	1	440	6.0	188.5
857	Q3uvv3	mus musculu	Q3UVV3_MOUSE	2	440	6.0	188.5
858	Q5z8w0	oryza sativ	Q5Z8W0_ORYSA	2	538	6.0	188.5
859	Q4sbu9	tetraodon n	Q4SBU9_TETNG	2	655	6.0	188.5
860	Q3kr19	homo sapien	Q3KR19_HUMAN	2	677	6.0	188.5
861	Q2vgy9	petromyzon	Q2VGY9_PETMA	2	218	6.0	188
862	Q32qr1	eptatretus	Q32QR1_EPTST	2	324	6.0	188
863	Q53hu6	homo sapien	Q53H06_HUMAN	2	368	6.0	188
864	O02678	canis famil	PGS1_CANFA	1	369	6.0	188
865	Q3uxk8	mus musculu	Q3UXK8_MOUSE	2	369	6.0	188
866	Q7tmw3	mus musculu	Q7TMW3_MOUSE	2	369	6.0	188
867	Q8k377	mus musculu	LRTM1_MOUSE	1	522	6.0	188
868	Q4se92	tetraodon n	Q4SE92_TETNG	2	626	6.0	188
869	Q5zih8	gallus gall	Q5ZIH8_CHICK	2	818	6.0	188
870	Q2vgr5	petromyzon	Q2VGR5_PETMA	2	195	6.0	187.5
871	Q4g1l0	eptatretus	Q4G1L0_EPTBU	2	259	6.0	187.5
872	Q9ddz8	petromyzon	Q9DDZ8_PETMA	2	310	6.0	187.5
873	Tsk	xenopus tro	TSK_XENTR	1	350	6.0	187.5
874	Q9h5g9	homo sapien	Q9H5G9_HUMAN	2	363	6.0	187.5
875	Q9vgh2	drosophila	Q9VGH2_DROME	2	425	6.0	187.5
876	Q7sxw3	brachydanio	LRC40_BRARE	1	601	6.0	187.5
877	Q4zj82	gallus gall	Q4ZJ82_CHICK	2	861	6.0	187.5
878	Q2xy22	drosophila	Q2XY22_DROYA	2	885	6.0	187.5
879	Q4g1k7	eptatretus	Q4G1K7_EPTST	2	260	6.0	187
880	Q4g1k0	eptatretus	Q4G1K0_EPTST	2	262	6.0	187
881	Q2ye79	eptatretus	Q2YE79_EPTST	2	324	6.0	187
882	Q61pg4	caenorhabdi	Q61PG4_CAEBR	2	592	6.0	187
883	Q9vz84	drosophila	Q9VZ84_DROME	2	615	6.0	187
884	Q6ei14	mus musculu	Q6EI14_MOUSE	2	735	6.0	187
885	Q16tw7	aedes aegyp	Q16TW7_AEDAE	2	807	6.0	187
886	Q5wa51	gallus gall	Q5WA51_CHICK	2	818	6.0	187
887	Q9tn0	pan paniscu	TLR4_PANPA	1	1741	6.0	187
888	Q5vzi9	homo sapien	Q5VZI9_HUMAN	2	193	5.9	186.5
889	Q32qv0	eptatretus	Q32QV0_EPTST	2	323	5.9	186.5
890	Q9ib75	xenopus lae	PGS1_XENLA	1	368	5.9	186.5
891	Q72u34	leptospira	Q72U34_LEPIC	2	521	5.9	186.5
892	Q1egj9	fugu rubrip	Q1EGJ9_FUGRU	2	536	5.9	186.5
893	Q5vzi7	homo sapien	Q5VZI7_HUMAN	2	639	5.9	186.5
894	Q5vzi8	homo sapien	Q5VZI8_HUMAN	2	799	5.9	186.5
895	O00206	homo sapien	TLR4_HUMAN	1	839	5.9	186.5
896	Q5lju2	drosophila	Q5LJU2_DROME	2	839	5.9	186.5
897	Q2vhc4	petromyzon	Q2VHC4_PETMA	2	839	5.9	186.5
898	Q2vgs1	petromyzon	Q2VGS1_PETMA	2	216	5.9	186
899	Q2vgr4	petromyzon	Q2VGR4_PETMA	2	218	5.9	186
900	Q6e4b4	petromyzon	Q6E4B4_PETMA	2	273	5.9	186
901	Q5ray4	pongo pygma	Q5RAY4_PONPY	2	368	5.9	186
902	P23515	homo sapien	OMGP_HUMAN	1	440	5.9	186
903	Q53hb8	homo sapien	Q53HB8_HUMAN	2	440	5.9	186
904	Q299n9	drosophila	Q299N9_DROPS	2	517	5.9	186
905	Q9vt44	drosophila	Q9VT44_DROME	2	552	5.9	186
906	Q9p2v4	homo sapien	LRC21_HUMAN	1	623	5.9	186
907	Q5i2m5	bos taurus	TLR9_BOVIN	1	1029	5.9	186
908	Q2vgv1	petromyzon	Q2VGV1_PETMA	2	185	5.9	185.5
909	Q2vgc6	petromyzon	Q2VGC6_PETMA	2	191	5.9	185.5
910	Q2vgr0	petromyzon	Q2VGR0_PETMA	2	191	5.9	185.5
911	Q2vgt6	petromyzon	Q2VGT6_PETMA	2	191	5.9	185.5
912	Q2vgx9	drosophila	Q2VGX9_PETMA	2	195	5.9	185.5
913	Q2ye24	eptatretus	Q2YE24_EPTST	2	251	5.9	185.5
914	Q4t3m1	tetraodon n	Q4T3M1_TETNG	2	369	5.9	185.5
915	Q66iw3	xenopus lae	Q66IW3_XENLA	2	466	5.9	185.5
916	Q297r4	drosophila	Q297R4_DROPS	2	795	5.9	185.5
917	Q6mf87	parachlamyd	Q6MF87_PARUW	2	953	5.9	185.5
918	Q4s4n7	tetraodon n	Q4S4N7_TETNG	2	254	5.9	185
919	Q32r21	eptatretus	Q32R21_EPTBU	2	323	5.9	185
920	Q6pbp5	brachydanio	Q6PBP5_BRARE	2	389	5.9	185
921	Q6pez8	homo sapien	Q6PEZ8_HUMAN	2	512	5.9	185
922	Q5zln0	gallus gall	LRC40_CHICK	1	603	5.9	185
923	Q4g1l5	eptatretus	Q4G1L5_EPTBU	2	257	5.9	184.5
924	Q2ye09	eptatretus	Q2YE09_EPTST	2	259	5.9	184.5
925	Q4kp09	lampetra ap	Q4KP09_LAMAP	2	270	5.9	184.5
926	Q17fy2	aedes aegyp	Q17FY2_AEDAE	2	608	5.9	184.5
927	Q5xwb9	equus cabal	Q5XWB9_HORSE	2	724	5.9	184.5
928	Q9v964	drosophila	Q9V964_DROME	2	799	5.9	184.5
929	Q69zv6	mus musculu	Q69ZV6_MOUSE	2	839	5.9	184.5
930	Q5f4k7	sus scrofa	Q5F4K7_PIG	2	841	5.9	184.5
931	Q2tnk4	sus scrofa	Q2TNK4_PIG	2	841	5.9	184.5
932	Q9myw3	equus cabal	TLR4_HORSE	1	843	5.9	184.5
933	Q810b7	mus musculu	SLIK5_MOUSE	1	957	5.9	184.5
934	Q65xs3	oryza sativ	Q65XS3_ORYSA	2	1007	5.9	184.5
935	Q5gq97	gallus gall	Q5GQ97_CHICK	2	1046	5.9	184.5
936	Q69jn6	oryza sativ	Q69JN6_ORYSA	2	1214	5.9	184.5
937	Q6e4m5	petromyzon	Q6E4M5_PETMA	2	187	5.9	184
938	Q2vgj6	mus musculu	Q2VGJ6_MOUSE	2	192	5.9	184
939	Q6e4k5	petromyzon	Q6E4K5_PETMA	2	253	5.9	184
940	Q6e4k7	petromyzon	Q6E4K7_PETMA	2	263	5.9	184
941	Q4g1m0	eptatretus	Q4G1M0_EPTBU	2	274	5.9	184
942	Q4rf21	tetraodon n	Q4RF21_TETNG	2	291	5.9	184
943	P21810	homo sapien	PGS1_HUMAN	1	368	5.9	184
944	Q53fi4	homo sapien	Q53FI4_HUMAN	2	368	5.9	184
945	Q3taf9	mouse	Q3TAF9_MOUSE	2	369	5.9	184
946	Q7qf76	anopheles g	Q7QF76_ANOGA	2	473	5.9	184
947	Q4rgc6	tetraodon n	Q4RGC6_TETNG	2	543	5.9	184
948	Q6k6x6	oryza sativ	Q6K6X6_ORYSA	2	552	5.9	184
949	Q7pjd0	anopheles g	Q7PJD0_ANOGA	2	565	5.9	184
950	Q810b8	mus musculu	SLIK4_MOUSE	1	837	5.9	184
951	Q3mnf2	bos taurus	Q3MNF2_BOVIN	2	1058	5.9	184
952	Q6e4f6	petromyzon	Q6E4F6_PETMA	2	187	5.9	183.5
953	Q9w2b9	drosophila	Q9W2B9_DROME	2	287	5.9	183.5
954	Q6nny6	brachydanio	Q6NNY6_BRARE	2	292	5.9	183.5
955	Q7q696	anopheles g	Q7Q696_ANOGA	2	652	5.9	183.5
956	Q6a0e8	mus musculu	Q6A0E8_MOUSE	2	727	5.9	183.5
957	Q9epq1	mus musculu	TLR1_MOUSE	1	795	5.9	183.5
958	Q5ggx1	sus scrofa	Q5GGX1_PIG	2	824	5.9	183.5
959	Q68y56	sus scrofa	TLR4_PIG	1	841	5.9	183.5
960	Q401c7	pig	Q401C7_PIG	2	841	5.9	183.5
961	Q2xy30	drosophila	Q2XY30_DROSI	2	864	5.9	183.5
962	Q2xy31	drosophila	Q2XY31_DROSI	2	867	5.9	183.5
963	Q2xy27	drosophila	Q2XY27_DROER	2	871	5.9	183.5
964	Q2xy28	drosophila	Q2XY28_DROYA	2	871	5.9	183.5
965	Q2xy29	drosophila	Q2XY29_DROYA	2	871	5.9	183.5
966	Q5zjd0	gallus gall	Q5ZJD0_CHICK	2	1059	5.9	183.5
967	Q2m1b0	drosophila	Q2M1B0_DROPS	2	1322	5.9	183.5
968	Q96nw7	homo sapien	LRRC7_HUMAN	1	1537	5.9	183.5
969	Q8bj09	mus musculu	Q8BJ09_MOUSE	2	432	5.8	183
970	Q9vu53	drosophila	Q9VU53_DROME	2	540	5.8	183
971	Q6p3y9	mus musculu	Q6P3Y9_MOUSE	2	568	5.8	183
972	Q14392	homo sapien	LRC32_HUMAN	1	662	5.8	183
973	Q7zt81	oncorhynchu	Q7ZT81_ONCMY	2	664	5.8	183
974	Q17gd6	aedes aegyp	Q17GD6_AEDAE	2	673	5.8	183
975	Q5zj34	gallus gall	Q5ZJ34_CHICK	2	972	5.8	183
976	Q6e4g7	petromyzon	Q6E4G7_PETMA	2	187	5.8	182.5
977	Q6e4g1	petromyzon	Q6E4G1_PETMA	2	187	5.8	182.5
978	Q2vgv7	drosophila	Q2VGV7_PETMA	2	219	5.8	182.5
979	Q4g1l8	eptatretus	Q4G1L8_EPTBU	2	257	5.8	182.5
980	Q2ye27	eptatretus	Q2YE27_EPTBU	2	261	5.8	182.5

No.	Score	pI	Len	Accession	Organism	Ct	Sequence ID
981	182.5	5.8	298	Q32qy7	eptatretus	2	Q32QY7_EPTBU
982	182.5	5.8	379	Q9bxn1	homo sapien	1	ASPN_HUMAN
983	182.5	5.8	380	Q5tbf3	homo sapien	2	Q5TBF3_HUMAN
984	182.5	5.8	384	Q6p528	homo sapien	2	Q6P528_HUMAN
985	182.5	5.8	618	Q1l8w7	brachydanio	2	Q1L8W7_BRARE
986	182.5	5.8	810	Q8t3j2	drosophila	2	Q8T3J2_DROME
987	182.5	5.8	811	Q9vk54	drosophila	2	Q9VK54_DROME
988	182.5	5.8	828	Q8spe9	pongo pygma	1	TLR4_PONPY
989	182.5	5.8	837	Q8spe8	gorilla gor	1	TLR4_GORGO
990	182.5	5.8	864	Q2xy32	drosophila	2	Q2XY32_DROME
991	182.5	5.8	880	P91643	drosophila	2	P91643_DROME
992	182.5	5.8	958	S1ik5	homo sapien	1	SLIK5_HUMAN
993	182.5	5.8	958	Q5vt81	homo sapien	2	Q5VT81_HUMAN
994	182.5	5.8	999	Q4qqh1	homo sapien	2	Q4QQH1_HUMAN
995	182.5	5.8	1041	Q17pv0	aedes aegyp	2	Q17PV0_AEDAE
996	182.5	5.8		Q3hj14	trichodeemi	2	Q3HJ14_TRIER
997	182	5.8	192	Q2vgf9	petromyzon	2	Q2VGF9_PETMA
998	182	5.8	194	Q2vgz0	petromyzon	2	Q2VGZ0_PETMA
999	182	5.8	205	Q4r9x7	tetraodon n	2	Q4R9X7_TETNG
1000	182	5.8	252	Q4g1l8	eptatretus	2	Q4G1L8_EPTST
1001	182	5.8	271	Q6e4c4	petromyzon	2	Q6E4C4_PETMA
1002	182	5.8	297	Q4ru73	tetraodon n	2	Q4RU73_TETNG
1003	182	5.8	319	Q32r34	eptatretus	2	Q32R34_EPTBU
1004	182	5.8	369	P21809	bos taurus	1	PGS1_BOVIN
1005	182	5.8	369	O46390	ovis aries	1	PGS1_SHEEP
1006	182	5.8	369	Q17qb0	bos taurus	2	Q17QB0_BOVIN
1007	182	5.8	373	Q5ri45	brachydanio	2	Q5RI45_BRARE
1008	182	5.8	373	Q803t1	brachydanio	2	Q803T1_BRARE
1009	182	5.8	428	Q8f3f8	leptospira	2	Q8F3F8_LEPIN
1010	182	5.8	532	O96671	drosophila	2	O96671_DROME
1011	182	5.8	678	Q7q550	anopheles g	2	Q7Q550_ANOGA
1012	182	5.8	1022	Q8hxv0	bos taurus	2	Q8HXV0_BOVIN
1013	182	5.8	1029	Q866b2	bos taurus	2	Q866B2_BOVIN
1014	181.5	5.8	180	Q8bpj0	mus musculu	2	Q8BPJ0_MOUSE
1015	181.5	5.8	185	Q2vgz9	petromyzon	2	Q2VGZ9_PETMA
1016	181.5	5.8	191	Q2vh42	petromyzon	2	Q2VH42_PETMA
1017	181.5	5.8	251	Q4g1k2	eptatretus	2	Q4G1K2_EPTST
1018	181.5	5.8	259	Q4g1j8	eptatretus	2	Q4G1J8_EPTST
1019	181.5	5.8	298	Q32r41	eptatretus	2	Q32R41_EPTBU
1020	181.5	5.8	357	P28675	gallus gall	1	PGS2_CHICK
1021	181.5	5.8	599	Q7t3h6	brachydanio	2	Q7T3H6_BRARE
1022	181	5.8	670	Q16p50	aedes aegyp	2	Q16P50_AEDAE
1023	181	5.8	699	Q61pg3	caenorhabdi	2	Q61PG3_CAEBR
1024	181	5.8	1434	Q17nj6	aedes aegyp	2	Q17NJ6_AEDAE
1025	181	5.8	2160	O13488	magnaporthe	2	O13488_MAGGR
1026	181	5.8		O13328	magnaporthe	2	O13328_MAGGR
1027	181	5.8	192	Q2vgy4	petromyzon	2	Q2VGY4_PETMA
1028	181	5.8	298	Q2ye69	eptatretus	2	Q2YE69_EPTST
1029	180.5	5.8	372	O46403	equus cabal	1	PGS1_HORSE
1030	180.5	5.8	569	Q7qip3	anopheles g	2	Q7QIP3_ANOGA
1031	180.5	5.8	1013	O81q10	oryza sativ	2	O8LQ10_ORYSA
1032	180.5	5.8	1333	Q7qi68	anopheles g	2	Q7QI68_ANOGA
1033	180.5	5.8	371	Q6glq6	xenopus lae	2	Q6GLQ6_XENLA
1034	180.5	5.8	385	Q8bmw6	mus musculu	2	Q8BMW6_MOUSE
1035	180.5	5.8	441	Q8i170	drosophila	2	Q8I170_DROVI
1036	180	5.8	522	Q5r7m3	pongo pygma	1	AMGO2_PONPY
1037	180	5.8	584	Q6pgx3	brachydanio	2	Q6PGX3_BRARE
1038	180	5.8	821	Q96py3	homo sapien	2	Q96PY3_HUMAN
1039	180	5.8	859	Q1zzx0	mus musculu	2	Q1ZZX0_MUSMM
1040	180	5.8	1376	Q16x81	aedes aegyp	2	Q16X81_AEDAE
1041	180	5.8	1443	Q9vjq0	drosophila	2	Q9VJQ0_DROME
1042	180	5.7	1460	Q5hz61	xenopus tro	2	Q5HZ61_XENTR
1043	180	5.7	192	Q2vh29	petromyzon	2	Q2VH29_PETMA
1044	180	5.7	250	Q4g1m2	eptatretus	2	Q4G1M2_EPTBU
1045	179.5	5.7	436	Q29fb4	drosophila	2	Q29FB4_DROPS
1046	179.5	5.7	522	Q5r6b1	drosophila	2	LRTM1_FONPY
1047	179.5	5.7	817	Q9vs84	drosophila	2	Q9VS84_DROME
1048	179.5	5.7	817	Q86p15	drosophila	2	Q86P15_DROME
1049	179.5	5.7	843	Q7ztg5	gallus gall	2	Q7ZTG5_CHICK
1050	179.5	5.7	869	Q4s0c1	tetraodon n	2	Q4S0C1_TETNG
1051	179.5	5.7	185	Q2vgi7	petromyzon	2	Q2VGI7_PETMA
1052	179.5	5.7	187	Q6e4d6	petromyzon	2	Q6E4D6_PETMA
1053	179.5	5.7	195	Q2vgp4	petromyzon	2	Q2VGP4_PETMA

No.	Score	pI	Len	Accession	Organism	Ct	Sequence ID
1054	179.5	5.7	585	Q61gx3	caenorhabdi	2	Q61GX3_CAEBR
1055	179.5	5.7	799	Q3bby2	macaca mula	2	Q3BBY2_MACMU
1056	179.5	5.7	820	Q5r3f8	homo sapien	2	Q5R3F8_HUMAN
1057	179.5	5.7	1117	Q6p1c6	mus musculu	1	LRIG3_MOUSE
1058	179.5	5.7	4283	Q9erv0	rattus norv	2	Q9ERV0_RAT
1059	179	5.7	192	Q2vh01	petromyzon	2	Q2VH01_PETMA
1060	179	5.7	192	Q2vgc7	petromyzon	2	Q2VGC7_PETMA
1061	179	5.7	194	Q2vgv8	petromyzon	2	Q2VGV8_PETMA
1062	179	5.7	262	Q2vh46	petromyzon	2	Q2VH46_PETMA
1063	179	5.7	273	Q2ye11	eptatretus	2	Q2YE11_EPTST
1064	179	5.7	314	Q6e4b8	petromyzon	2	Q6E4B8_PETMA
1065	179	5.7	534	Q5m8m9	mus musculu	2	LRC52_MOUSE
1066	179	5.7	700	Q9vt89	drosophila	2	Q9VT89_DROME
1067	179	5.7	742	Q9p244	homo sapien	2	Q9P244_HUMAN
1068	179	5.7	815	Q9bjd4	strongyloce	2	Q9BJD4_STRPU
1069	179	5.7	905	Q17ld1	aedes aegyp	2	Q17LD1_AEDAE
1070	179	5.7	905	Q99mb1	mus musculu	1	TLR3_MOUSE
1071	179	5.7	969	Q499f3	mus musculu	2	Q499F3_MOUSE
1072	179	5.7	1029	Q41bc9	oncorhynchu	2	Q4LBC9_ONCMY
1073	179	5.7		Q5i2m4	ovis aries	1	TLR9_SHEEP
1074	178.5	5.7	161	Q2vh51	petromyzon	2	Q2VH51_PETMA
1075	178.5	5.7	176	Q56715	brachydanio	2	Q567L5_BRARE
1076	178.5	5.7	190	Q6e4d8	petromyzon	2	Q6E4D8_PETMA
1077	178.5	5.7	348	Q5r143	brachydanio	2	Q5R143_BRARE
1078	178.5	5.7	356	Q9de68	coturnix co	1	PGS2_COTJA
1079	178.5	5.7	443	Q67vv7	oryza sativ	2	Q67VV7_ORYSA
1080	178.5	5.7	493	O86wk6	homo sapien	1	AMGO1_HUMAN
1081	178.5	5.7	587	Q4qgj9	leishmania	2	Q4QGJ9_LEIMA
1082	178.5	5.7	1024	Q9rbs2	ralstonia s	1	Q9RBS2_RALSO
1083	178.5	5.7	1063	Q5z666	oryza sativ	2	Q5Z666_ORYSA
1084	178.5	5.7	1104	Q7xuh4	oryza sativ	2	Q7XUH4_ORYSA
1085	178.5	5.7	1107	Q3md20	anabaena va	2	Q3MD20_ANAVT
1086	178.5	5.7	1310	Q7tt36	mus musculu	1	GP125_MOUSE
1087	178	5.7	187	Q6e4h4	petromyzon	2	Q6E4H4_PETMA
1088	178	5.7	192	Q2vh53	petromyzon	2	Q2VH53_PETMA
1089	178	5.7	194	Q2vh56	petromyzon	2	Q2VH56_PETMA
1090	178	5.7	231	Q2vge4	petromyzon	2	Q2VGE4_PETMA
1091	178	5.7	298	Q3tv01	mus musculu	1	Q3TV01_MOUSE
1092	178	5.7	319	Q32qx9	eptatretus	2	Q32QX9_EPTST
1093	178	5.7	364	Q32qx4	eptatretus	2	Q32QX4_EPTST
1094	178	5.7	391	Q32qz3	eptatretus	2	Q32QZ3_EPTBU
1095	178	5.7	488	Q4rqi1	tetraodon n	2	Q4RQI1_TETNG
1096	178	5.7	522	Q4rxq5	tetraodon n	2	Q4RXQ5_TETNG
1097	178	5.7	578	Q86ue6	homo sapien	2	Q86UE6_HUMAN
1098	178	5.7	894	Q28ce3	xenopus tro	2	Q28CE3_XENTR
1099	178	5.7		Q9bjd6	strongyloce	2	Q9BJD6_STRPU
1100	178	5.7	187	Q9nyk1	homo sapien	1	TLR7_HUMAN
1101	178	5.7	192	Q9y4c4	homo sapien	2	Q9Y4C4_HUMAN
1102	178	5.7	1049	Q7pnf8	anopheles g	2	Q7PNF8_ANOGA
1103	178	5.7	1052	Q2vh41	petromyzon	2	Q2VH41_PETMA
1104	177.5	5.6	1257	Q2vgd7	petromyzon	2	Q2VGD7_PETMA
1105	177.5	5.6	195	Q2vgs6	petromyzon	2	Q2VGS6_PETMA
1106	177.5	5.6	215	Q4g1k5	eptatretus	2	Q4G1K5_EPTST
1107	177.5	5.6	275	Q4ldr7	sus scrofa	2	Q4LDR7_PIG
1108	177.5	5.6	796	Q59hi9	sus scrofa	2	Q59HI9_PIG
1109	177.5	5.6	796	Q4rmq1	tetraodon n	2	Q4RMQ1_TETNG
1110	177.5	5.6	809	Q5smw2	oryza sativ	2	Q5SMW2_ORYSA
1111	177.5	5.6	1026	P58681	mus musculu	1	TLR7_MOUSE
1112	177.5	5.6	1050	Q548j0	drosophila	2	Q548J0_DROME
1113	177.5	5.6	1360	Q7kta0	drosophila	2	Q7KTA0_DROME
1114	177.5	5.6	2300	Q01631	neurospora	1	CYAA_NEUCR
1115	177.5	5.6	2493	P49606	ustilago ma	1	CYAA_USTMA
1116	177.5	5.6	2493	Q4p3t1	ustilago ma	2	Q4P3T1_USTMA
1117	177.5	5.6	187	Q6e4h5	petromyzon	2	Q6E4H5_PETMA
1118	177	5.6	192	Q2vh26	petromyzon	2	Q2VH26_PETMA
1119	177	5.6	192	Q2vgq0	petromyzon	2	Q2VGQ0_PETMA
1120	177	5.6	192	Q2vgr6	petromyzon	2	Q2VGR6_PETMA
1121	177	5.6	192	Q2vgw2	petromyzon	2	Q2VGW2_PETMA
1122	177	5.6	192	Q2vh28	petromyzon	2	Q2VH28_PETMA
1123	177	5.6	334	Q4sbu8	tetraodon n	2	Q4SBU8_TETNG
1124	177	5.6	343	Q9de67	coturnix co	1	LUM_COTJA
1125	177	5.6	615	Q29ea2	drosophila	2	Q29EA2_DROPS

#	Score	E	Length	N	Accession	Code	Organism
1127	177	5.6	662	1	LRC32_PONPY	Q5rf01	pongo pygma
1128	177	5.6	666	1	Q7Q2W6_ANOGA	Q7q2w6	anopheles g
1129	177	5.6	670	2	Q5FW85_MOUSE	Q5fw85	m extracell
1130	177	5.6	1370	2	Q58NA4_APIME	Q58na4	apis mellif
1131	176.5	5.6	185	2	Q2VGE5_PETMA	Q2vge5	petromyzon
1132	176.5	5.6	187	2	Q6E4M0_PETMA	Q6e4m0	petromyzon
1133	176.5	5.6	195	2	Q2VGT9_PETMA	Q2vgt9	petromyzon
1134	176.5	5.6	322	2	Q32R02_EPTST	Q32r02	eptatretus
1135	176.5	5.6	520	2	Q5VR46_ORYSA	Q5vr46	oryza sativ
1136	176.5	5.6	522	1	AMGO2_HUMAN	Q86j2	homo sapien
1137	176.5	5.6	522	2	Q4VBP6_HUMAN	Q4vbp6	homo sapien
1138	176.5	5.6	628	2	Q7PVZ6_ANOGA	Q7pvz6	anopheles g
1139	176.5	5.6	856	2	Q59HI7_PIG	Q59hi7	sus scrofa
1140	176.5	5.6	901	1	Q4SBD4_TETNG	Q4sbd4	tetraodon n
1141	176.5	5.6	1495	1	LRRC7_RAT	P70587	rattus norv
1142	176	5.6	220	2	Q2VH09_PETMA	Q2vh09	petromyzon
1143	176	5.6	249	2	Q4SUM4_TETNG	Q4sum4	tetraodon n
1144	176	5.6	503	2	Q8LJ87_ORYSA	Q81j87	oryza sativ
1145	176	5.6	623	2	Q95S21_DROME	Q95s21	drosophila
1146	176	5.6	862	2	Q5GR02_CHICK	Q5gr02	gallus gall
1147	176	5.6	904	2	Q5TJ59_BOVIN	Q5tj59	bos taurus
1148	176	5.6	905	2	Q5TJ58_BOVIN	Q5tj58	bos taurus
1149	176	5.6	906	2	Q4SRZ0_TETNG	Q4srz0	tetraodon n
1150	176	5.6	913	2	Q1PA38_ONCMY	Q1pa38	oncorhynchu
1151	176	5.6	1032	1	TLR9_CANFA	Q5i2m8	canis famil
1152	175.5	5.6	1257	2	Q9VK28_DROME	Q9vk28	drosophila
1153	176	5.6	1412	2	LAP2_HUMAN	Q96rt1	homo sapien
1154	175.5	5.6	167	2	Q2VGJ8_PETMA	Q2vgj8	petromyzon
1155	175.5	5.6	185	2	Q2VGW3_PETMA	Q2vgw3	petromyzon
1156	175.5	5.6	251	2	Q2YE03_EPTST	Q2ye03	eptatretus
1157	175.5	5.6	272	2	Q4KP14_9PETR	Q4kp14	ichthyomyzo
1158	175.5	5.6	324	2	Q32R05_EPTST	Q32r05	eptatretus
1159	175.5	5.6	384	2	Q4T0V4_TETNG	Q4t0v4	tetraodon n
1160	175.5	5.6	440	2	Q7TNM3_RAT	Q7tnm3	rattus norv
1161	175	5.6	492	1	AMGO1_MOUSE	Q80zd8	mus musculu
1162	175	5.6	816	2	Q29168_DROPS	Q29168	drosophila
1163	175.5	5.6	841	2	Q2V898_BOSTR	Q2v898	boselaphus
1164	175.5	5.6	1017	2	Q5H718_FUGRU	Q5h718	fugu rubrip
1165	175.5	5.6	1490	1	LRRC7_MOUSE	Q80te7	mus musculu
1166	175.5	5.6	1731	1	Q4S0D3_TETNG	Q4s0d3	tetraodon n
1167	175	5.6	168	2	Q2VHC0_PETMA	Q2vhc0	petromyzon
1168	175	5.6	192	2	Q2VH74_PETMA	Q2vh74	petromyzon
1169	175	5.6	192	2	Q2VGK6_PETMA	Q2vgk6	petromyzon
1170	175	5.6	252	2	Q4G1J2_EPTST	Q4g1j2	eptatretus
1171	175	5.6	297	2	Q32QZ0_EPTBU	Q32qz0	eptatretus
1172	175	5.6	323	2	Q32R31_EPTBU	Q32r31	eptatretus
1173	175	5.6	343	1	LUM_CHICK	P51890	gallus gall
1174	174.5	5.6	474	2	Q290X6_DROPS	Q290x6	drosophila
1175	174.5	5.6	510	2	Q9BGY6_MACFA	Q9bgy6	macaca fasc
1176	174.5	5.6	512	1	Q17F18_AEDAE	Q17f18	aedes aegyp
1177	174.5	5.6	905	2	Q3TM31_MOUSE	Q3tm31	mus musculu
1178	174.5	5.6	941	2	Q5H722_FUGRU	Q5h722	fugu rubrip
1179	175	5.6	973	2	Q6KCC7_ONCMY	Q6kcc7	oncorhynchu
1180	175	5.6	1031	2	Q2EEY0_HORSE	Q2eey0	equus cabal
1181	175	5.6	1137	2	Q7QHH1_ANOGA	Q7qhh1	anopheles g
1182	174.5	5.6	190	2	Q6E4E5_PETMA	Q6e4e5	petromyzon
1183	174.5	5.6	191	2	Q2VGI5_PETMA	Q2vgi5	petromyzon
1184	174.5	5.6	193	2	Q2VGD0_PETMA	Q2vgd0	petromyzon
1185	174.5	5.6	440	2	Q4J5V4_AZOVI	Q4j5v4	azotobacter
1186	174.5	5.6	512	2	Q9CQ76_MOUSE	Q9cq76	mus musculu
1187	174.5	5.6	567	2	Q4SL10_TETNG	Q4sl10	tetraodon n
1188	174.5	5.6	602	1	LRC40_MOUSE	Q6gpj5	mus musculu
1189	174.5	5.6	605	1	LRC40_XENLA	Q9epw9	xenopus lae
1190	174.5	5.6	795	1	TLR6_MOUSE		mus musculu
1191	174.5	5.6	806	2	Q3UV88_MOUSE	Q3uv88	mus musculu
1192	174.5	5.6	1020	2	Q5ZED4_ORYSA	Q5zed4	oryza sativ
1193	174.5	5.6	1060	2	Q6ZGM3_ORYSA	Q6zgm3	oryza sativ
1194	174	5.6	194	2	Q2VH35_PETMA	Q2vh35	petromyzon
1195	174	5.6	196	2	Q2VGF0_PETMA	Q2vgf0	petromyzon
1196	174	5.6	299	2	Q32R28_EPTBU	Q32r28	eptatretus
1197	174	5.6	490	2	Q4RYL5_TETNG	Q4ryl5	tetraodon n
1198	174	5.6	535	2	Q8RX50_BRANI	Q8rx50	brassica ni
1199	174	5.6	544	2	Q7Q2W5_ANOGA	Q7q2w5	anopheles g
1200	174	5.6	651	2	Q4JQQ2_XENLA	Q4jqq2	xenopus lae
1201	174	5.6	859	2	TLR5_MOUSE	Q9jlf7	mus musculu
1202	174	5.6	913	2	Q3KUR8_ONCMY	Q3kur8	oncorhynchu
1203	174	5.6	951	1	LGR4_RAT	Q92h4	rattus norv
1204	174	5.6	1361	2	Q17FX0_AEDAE	Q17fx0	aedes aegyp
1205	174	5.6	1367	2	Q1RMC9_HUMAN	Q1rmc9	homo sapien
1206	174	5.6	1371	2	Q1RMD0_HUMAN	Q1rmd0	homo sapien
1207	173.5	5.5	161	2	Q2VH22_PETMA	Q2vh22	petromyzon
1208	173.5	5.5	261	2	Q5M8T1_HUMAN	Q5m8t1	homo sapien
1209	173.5	5.5	337	2	Q4RJX0_TETNG	Q4rjx0	tetraodon n
1210	173.5	5.5	353	2	Q640B1_XENTR	Q640b1	xenopus tro
1211	173.5	5.5	364	2	Q6GNX8_XENLA	Q6gnx8	xenopus lae
1212	173.5	5.5	421	1	OMD_HUMAN	Q99983	homo sapien
1213	173.5	5.5	421	2	Q5TBF4_HUMAN	Q5tbf4	homo sapien
1214	173.5	5.5	440	2	Q7TQ25_RAT	Q7tq25	rattus norv
1215	173.5	5.5	537	1	LGI4_MOUSE	Q8kls1	mus musculu
1216	173.5	5.5	537	2	Q3UYI9_MOUSE	Q3uyi9	mus musculu
1217	173.5	5.5	727	2	Q6GV21_BOVIN	Q6gv21	bos taurus
1218	173.5	5.5	806	2	Q7TPC5_MOUSE	Q7tpc5	mus musculu
1219	173.5	5.5	826	2	TLR4_PAPAN	Q9tsp2	papio anubi
1220	173.5	5.5	884	2	Q5H720_FUGRU	Q5h720	fugu rubrip
1221	173.5	5.5	1167	2	Q16XG0_AEDAE	Q16xg0	aedes aegyp
1222	173.5	5.5	1681	2	Q299Y2_DROPS	Q299y2	drosophila
1223	173	5.5	168	2	Q2VGX8_PETMA	Q2vgx8	petromyzon
1224	173	5.5	192	2	Q2VHA2_PETMA	Q2vha2	petromyzon
1225	173	5.5	192	2	Q2VGG5_PETMA	Q2vgg5	petromyzon
1226	173	5.5	194	2	Q2VHC8_PETMA	Q2vhc8	petromyzon
1227	173	5.5	252	2	Q4GLI4_EPTST	Q4gli4	eptatretus
1228	173	5.5	269	2	Q6E4C2_PETMA	Q6e4c2	eptatretus
1229	173	5.5	360	1	PGS2_HORSE	O46542	equus cabal
1230	173	5.5	470	2	Q9V354_DROME	Q9v354	drosophila
1231	173	5.5	539	2	Q503F6_BRARE	Q503f6	brachydanio
1232	173	5.5	664	2	Q5UT54_SALSA	Q5ut54	salmo salar
1233	173	5.5	853	2	Q8CB40_MOUSE	Q8cb40	mus musculu
1234	173	5.5	892	1	Q466H0_METBF	Q466h0	methanosarc
1235	173	5.5	925	1	GLHR_ANTEL	P35409	anthopleura
1236	173	5.5	1459	2	Q7Q0C5_ANOGA	Q7q0c5	anopheles g
1237	173	5.5	1459	2	Q8WRE4_ANOGA	Q8wre4	anopheles g
1238	172.5	5.5	161	2	Q2VHB2_PETMA	Q2vhb2	petromyzon
1239	172.5	5.5	163	2	Q2VGH1_PETMA	Q2vgh1	petromyzon
1240	172.5	5.5	171	2	Q6E4E2_PETMA	Q6e4e2	petromyzon
1241	172.5	5.5	237	2	Q2VHC2_PETMA	Q2vhc2	petromyzon
1242	172.5	5.5	259	2	Q2YE13_EPTST	Q2ye13	eptatretus
1243	172.5	5.5	353	2	Q2YE22_EPTST	Q2ye22	eptatretus
1244	172.5	5.5	353	1	KERA_CHICK	O42235	gallus gall
1245	172.5	5.5	359	1	KERA_COTJA	Q9de66	coturnix co
1246	172.5	5.5	359	2	PGS2_HUMAN	P07585	homo sapien
1247	172.5	5.5	378	1	PGS2_PANTR	Q5r1v9	pan troglod
1248	172.5	5.5	739	2	Q6FH10_HUMAN	Q6fh10	homo sapien
1249	172.5	5.5	823	2	Q5R294_DROSI	Q5r294	drosophila
1250	172.5	5.5	1851	2	Q60NV9_CABBR	Q60nv9	caenorhabdi
1251	172.5	5.5	4256	1	Q68FM6_MOUSE	Q68fm6	mus musculu
1252	172.5	5.5	339	2	Q8CCW8_MOUSE	Q8ccw8	mus musculu
1253	172.5	5.5	347	1	LAP4_DROME	Q7kry7	drosophila
1254	172.5	5.5	411	2	Q8MJF3_CANFA	Q8mjf3	canis famil
1255	172	5.5	577	2	Q4SU68_TETNG	Q4su68	tetraodon n
1256	172	5.5	904	1	TSK_BRARE	Q58a48	brachydanio
1257	172	5.5	1134	2	Q4S9P3_TETNG	Q4s9p3	tetraodon n
1258	172	5.5	1693	2	Q8N3K5_HUMAN	Q8n3k5	homo sapien
1259	172	5.5	171	2	Q1G1A3_BUBBU	Q1g1a3	bubalus bub
1260	172	5.5	193	1	O65510_ARATH	O65510	arabidopsis
1261	171.5	5.5	195	2	Q4INH4_GIBZE	Q4inh4	gibberella
1262	171.5	5.5	605	2	Q2VGJ0_PETMA	Q2vgj0	petromyzon
1263	171.5	5.5	683	2	Q2VHD1_PETMA	Q2vhd1	petromyzon
1264	171.5	5.5	791	2	Q2VH57_PETMA	Q2vh57	petromyzon
1265	171.5	5.5	858	2	Q9V900_DROME	Q9v900	drosophila
1266	171.5	5.5	858	1	LRC40_XENTR	Q5m8g4	xenopus tro
1267	171.5	5.5	858	2	LRCH4_HUMAN	O75427	homo sapien
1268	171.5	5.5		1	Q2L8H0_LISMO	Q2l8h0	listeria mo
1269	171.5	5.5		1	LRC8D_RAT	Q5u308	rattus norv
1270	171.5	5.5		2	TLR5_HUMAN	O60602	homo sapien
1271	171.5	5.5		2	Q32MI3_HUMAN	Q32mi3	homo sapien
1272	171.5	5.5		2	Q32MI2_HUMAN	Q32mi2	homo sapien

No.	Value	Score	Length	n	Protein ID	Accession	Organism
1273	171.5	5.5	859	1	LRC8D_MOUSE	Q8bgr2	mus musculu
1274	171.5	5.5	859	2	Q3TI70_MOUSE	Q3ti70	mus musculu
1275	171.5	5.5	1589	2	Q9UUQ9_METAN	Q9uuq9	metarhizium
1276	171	5.5	168	2	Q2VHF6_PETMA	Q2vhf6	petromyzon
1277	171	5.5	192	2	Q2VGZ1_PETMA	Q2vgz1	petromyzon
1278	171	5.5	194	2	Q2VGS3_PETMA	Q2vgs3	petromyzon
1279	171	5.5	299	2	Q32Q27_EPTBU	Q32q27	eptatretus
1280	171	5.5	354	2	Q3TSV1_MOUSE	Q3tsv1	mus musculu
1281	171	5.5	360	1	PGS2_PIG	Q9xsd9	sus scrofa
1282	171	5.5	360	2	Q6DVI1_GECJA	Q6dvi1	gecko japon
1283	171	5.5	469	2	Q3URB9_MOUSE	Q3urb9	mus musculu
1284	171	5.5	512	2	Q17F19_AEDAE	Q17f19	aedes aegyp
1285	171	5.5	517	2	Q17K69_AEDAE	Q17k69	aedes aegyp
1286	171	5.5	643	2	Q502J4_BRARE	Q502j4	brachydanio
1287	171	5.5	833	1	TLR4_FELCA	P58727	felis silve
1288	171	5.5	976	2	Q3V1N1_MOUSE	Q3v1n1	mus musculu
1289	171	5.5	976	2	Q3TAN2_MOUSE	Q3tan2	mus musculu
1290	171	5.5	1091	2	Q17L59_AEDAE	Q17l59	aedes aegyp
1291	171	5.5	1317	2	Q5TUS9_ANOGA	Q5tus9	anopheles g
1292	170.5	5.4	185	2	Q2VGH0_PETMA	Q2vgh0	petromyzon
1293	170.5	5.4	246	2	Q6E4J1_PETMA	Q6e4j1	petromyzon
1294	170.5	5.4	359	2	Q4R5D2_MACFA	Q4r5d2	macaca fasc
1295	170.5	5.4	373	1	ASPN_MOUSE	Q99mq4	mus musculu
1296	170.5	5.4	741	2	Q8KTF7_LISMO	Q8ktf7	listeria mo
1297	170.5	5.4	761	2	Q3XNG0_9PROT	Q3xng0	magnetococc
1298	170.5	5.4	794	2	Q2L8H9_LISMO	Q2l8h9	listeria mo
1299	170.5	5.4	1031	1	TLR9_FELCA	Q512m7	felis silve
1300	170.5	5.4	2145	1	CYAA_PODAN	Q01513	podospora a
1301	170	5.4	187	2	Q6E4D9_PETMA	Q6e4d9	petromyzon
1302	170	5.4	192	2	Q2VGM4_PETMA	Q2vgm4	petromyzon
1303	170	5.4	192	2	Q2VH20_PETMA	Q2vh20	petromyzon
1304	170	5.4	192	2	Q2VGG2_PETMA	Q2vgg2	petromyzon
1305	170	5.4	364	2	Q2VGI9_PETMA	Q2vgi9	petromyzon
1306	170	5.4	415	1	LRC19_MOUSE	Q295b8	mus musculu
1307	170	5.4	473	2	Q295B8_DROPS	Q295b8	drosophila
1308	170	5.4	545	2	Q3TSQ1_MOUSE	Q3tsq1	mus musculu
1309	170	5.4	572	2	Q1EGK2_FUGRU	Q1egk2	fugu rubrip
1310	170	5.4	883	2	Q4QGJ6_LEIMA	Q4qgj6	leishmania
1311	170	5.4	907	2	Q4VAM0_HUMAN	Q4vam0	homo sapien
1312	170	5.4	1024	1	LGR5_HUMAN	O75473	homo sapien
1313	170	5.4	1032	2	Q4VAM2_HUMAN	Q4vam2	homo sapien
1314	170	5.4	167	2	Q84IE6_RALSO	Q84ie6	ralstonia s
1315	170	5.4	173	2	Q59ER8_HUMAN	Q59er8	homo sapien
1316	169.5	5.4	352	2	Q2VGL5_PETMA	Q2vgl5	petromyzon
1317	169.5	5.4	366	2	Q2VGD2_PETMA	Q2vgd2	petromyzon
1318	169.5	5.4	463	1	KERA_BOVIN	O62702	bos taurus
1319	169.5	5.4	493	2	Q8BX06_MOUSE	Q8bx06	mus musculu
1320	169.5	5.4	651	2	Q2LYW7_DROPS	Q2lyw7	drosophila
1321	169.5	5.4	760	1	AMGO1_RAT	Q80zd7	rattus norv
1322	169.5	5.4	876	2	Q4T8T9_TETNG	Q4t8t9	tetraodon n
1323	169.5	5.4	991	2	Q9T0K5_ARATH	Q9t0k5	arabidopsis
1324	169.5	5.4	1271	2	Q67WE5_ORYSA	Q67we5	oryza sativ
1325	169.5	5.4	1545	1	FLII_MOUSE	Q9jj28	mus musculu
1326	169	5.4	168	2	Q29P78_DROPS	Q29p78	drosophila
1327	169	5.4	217	2	Q2VGQ9_PETMA	Q2vgq9	petromyzon
1328	169	5.4	273	2	Q66WJ6_FELCA	Q66wj6	felis silve
1329	169	5.4	279	2	Q5XPY6_ICTPU	Q5xpy6	ictalurus p
1330	169	5.4	354	2	Q58HK2_TRASC	Q58hk2	trachemys s
1331	169	5.4	360	1	PGS2_MOUSE	P28654	mus musculu
1332	169	5.4	757	2	Q3UKR1_MOUSE	Q3ukr1	mus musculu
1333	169	5.4	839	2	Q6J0Y6_PAROL	Q6j0y6	paralichthy
1334	169	5.4	1175	2	Q69MS7_ORYSA	Q69ms7	oryza sativ
1335	169	5.4	1288	2	Q9RX57_DEIRA	Q9rx57	deinococcus
1336	169	5.4	1658	2	Q4RER3_TETNG	Q4rer3	tetraodon n
1337	168.5	5.4	169	2	Q624K5_CAEBR	Q624k5	caenorhabdi
1338	168.5	5.4	184	2	Q4PLE9_GIBIN	Q4ple9	gibberella
1339	168.5	5.4	185	2	Q2VH97_PETMA	Q2vh97	petromyzon
1340	168.5	5.4	246	2	Q2VGY2_PETMA	Q2vgy2	petromyzon
1341	168.5	5.4	255	2	Q2VGQ5_PETMA	Q2vgq5	petromyzon
1342	168.5	5.4	333	2	Q4KP10_LAMAP	Q4kp10	lampetra ap
1343	168.5	5.4		2	Q66WJ3_FELCA	Q66wj3	felis silve
1344	168.5	5.4		2	Q4SY28_TETNG	Q4sy28	tetraodon n

No.	Value	Score	Length	n	Protein ID	Accession	Organism
1346	168.5	5.4	343	2	Q50LS3_BRARE	Q50ls3	brachydanio
1347	168.5	5.4	353	2	Q7SYS8_XENLA	Q7sys8	xenopus lae
1348	168.5	5.4	363	2	Q8C8A7_MOUSE	Q8c8a7	mus musculu
1349	168.5	5.4	366	2	Q3UGP9_MOUSE	Q3ugp9	mus musculu
1350	168.5	5.4	378	2	Q5R264_DROSE	Q5r264	drosophila
1351	168.5	5.4	619	2	Q6K8K0_ORYSA	Q6k8k0	oryza sativ
1352	168.5	5.4	685	2	Q6T545_LISMO	Q6t545	listeria mo
1353	168.5	5.4	694	2	Q61P91_CAEBR	Q61p91	caenorhabdi
1354	168.5	5.4	728	2	Q6T546_LISMO	Q6t546	listeria mo
1355	168.5	5.4	744	2	Q8KTF6_LISMO	Q8ktf6	listeria mo
1356	168.5	5.4	791	2	Q2L8H6_LISMO	Q2l8h6	listeria mo
1357	168.5	5.4	800	2	Q4EQX8_LISMO	Q4eqx8	listeria mo
1358	168.5	5.4	907	1	LGR5_MOUSE	Q9z1p4	mus musculu
1359	168.5	5.4	1036	2	Q9FN37_ARATH	Q9fn37	arabidopsis
1360	168.5	5.4	1360	2	Q9NDI1_DROME	Q9ndi1	drosophila
1361	168.5	5.4	1724	2	Q4H4B6_BRARE	Q4h4b6	brachydanio
1362	168.5	5.4	3201	2	Q2QBE0_9ALPH	Q2qbe0	cercopithec
1363	168	5.4	351	2	Q32N68_XENLA	Q32n68	xenopus lae
1364	168	5.4	351	2	Q65YW8_XENLA	Q65yw8	xenopus lae
1365	168	5.4	369	2	Q28X02_DROPS	Q28x02	drosophila
1366	168	5.4	402	2	Q72U35_LEPIC	Q72u35	leptospira
1367	168	5.4	539	2	Q16K00_AEDAE	Q16k00	aedes aegyp
1368	168	5.4	773	2	Q5NE35_LISMO	Q5ne35	listeria mo
1369	168	5.4	951	1	LGR4_HUMAN	Q9hbx1	homo sapien
1370	168	5.4	977	2	Q8GVW0_ORYSA	Q8gvw0	oryza sativ
1371	168	5.4	1050	2	Q2L4T3_CANFA	Q2l4t3	canis famil
1372	167.5	5.4	147	2	Q9TT00_PIG	Q9tt00	sus scrofa
1373	167.5	5.3	171	2	Q2VHC1_PETMA	Q2vhc1	petromyzon
1374	167.5	5.3	185	2	Q2VGV4_PETMA	Q2vgv4	petromyzon
1375	167.5	5.3	351	1	KERA_MOUSE	O35367	mus musculu
1376	167.5	5.3	360	1	PGS2_SHEEP	Q9tte2	ovis aries
1377	167.5	5.3	378	2	Q72U36_LEPIC	Q72u36	leptospira
1378	167.5	5.3	396	2	Q8C3D9_MOUSE	Q8c3d9	mus musculu
1379	167.5	5.3	422	1	OMD_BOVIN	O77742	bos taurus
1380	167.5	5.3	550	2	Q2QXR6_ORYSA	Q2qxr6	oryza sativ
1381	167.5	5.3	568	2	Q16M66_AEDAE	Q16m66	aedes aegyp
1382	167.5	5.3	694	2	Q4RYL2_TETNG	Q4ryl2	tetraodon n
1383	167.5	5.3	907	2	Q3VIL2_MOUSE	Q3vil2	mus musculu
1384	167.5	5.3	917	2	Q75GM9_ORYSA	Q75gm9	oryza sativ
1385	167.5	5.3	1174	2	Q25AQ0_ORYSA	Q25aq0	oryza sativ
1386	167.5	5.3	1174	2	Q7XS37_ORYSA	Q7xs37	oryza sativ
1387	167.5	5.3	1225	2	Q16VI7_AEDAE	Q16vi7	aedes aegyp
1388	167	5.3	168	2	Q2VGM8_PETMA	Q2vgm8	petromyzon
1389	167	5.3	262	2	Q2YE18_EPTST	Q2ye18	eptatretus
1390	167	5.3	537	2	Q6P2A4_RAT	Q6p2a4	rattus norv
1391	167	5.3	582	2	Q6AYI5_RAT	Q6ayi5	rattus norv
1392	167	5.3	633	2	Q8F3F6_LEPIN	Q8f3f6	leptospira
1393	167	5.3	743	2	Q84CF7_LISMO	Q84cf7	listeria mo
1394	167	5.3	744	2	Q8KTF4_LISMO	Q8ktf4	listeria mo
1395	167	5.3	777	2	Q28ZP9_DROPS	Q28zp9	drosophila
1396	167	5.3	794	2	Q6YW99_ORYSA	Q6yw99	oryza sativ
1397	167	5.3	838	1	TLR4_CRIGR	Q9wv82	cricetulus
1398	167	5.3	886	2	Q469S7_METBF	Q46987	methanosarc
1399	167	5.3	939	2	Q4SZU0_TETNG	Q4szu0	tetraodon n
1400	167	5.3	1112	2	Q4G2W2_LYCPM	Q4g2w2	lycopersico
1401	167	5.3	1112	2	Q41397_LYCPM	Q41397	lycopersico
1402	167	5.3	1112	2	Q41398_LYCPM	Q41398	lycopersico
1403	167	5.3	1263	2	Q4SID1_TETNG	Q4sid1	tetraodon n
1404	167	5.3	1845	2	Q5QNQ9_MOUSE	Q5qnq9	mus musculu
1405	166.5	5.3	185	2	Q2VGJ9_PETMA	Q2vgj9	petromyzon
1406	166.5	5.3	351	2	Q3KQ16_XENLA	Q3kq16	xenopus lae
1407	166.5	5.3	370	2	Q32BN5_BOVIN	Q32bn5	bos taurus
1408	166.5	5.3	483	2	Q5NE36_LISMO	Q5ne36	listeria mo
1409	166.5	5.3	549	2	Q9SVW8_ARATH	Q9svw8	arabidopsis
1410	166.5	5.3	582	2	Q5R423_PONPY	Q5r423	pongo pygma
1411	166.5	5.3	601	2	Q16P98_AEDAE	Q16p98	aedes aegyp
1412	166.5	5.3	739	2	Q84CF6_LISMO	Q84cf6	listeria mo
1413	166.5	5.3	741	2	Q8KTF0_LISMO	Q8ktf0	listeria mo
1414	166.5	5.3	741	2	Q8KTF9_LISMO	Q8ktf9	listeria mo
1415	166.5	5.3	743	2	Q9SRV9_DROME	Q9srv9	drosophila
1416	166.5	5.3	743	2	Q8KTF2_LISMO	Q8ktf2	listeria mo
1417	166.5	5.3	744	2	Q8KTF1_LISMO	Q8ktf1	listeria mo

Left column table:

#	acc		val	5.x	code	species
1419	744	2	166.5	5.3	Q8KTF5_LISMO	Q8ktf5 listeria mo
1420	744	2	166.5	5.3	Q8KTF8_LISMO	Q8ktf8 listeria mo
1421	744	2	166.5	5.3	Q8KHN1_LISMO	Q8khn1 listeria mo
1422	744	2	166.5	5.3	Q8KI88_LISMO	Q8ki88 listeria mo
1423	746	2	166.5	5.3	Q8KTF3_LISMO	Q8ktf3 listeria mo
1424	792	2	166.5	5.3	Q5NE37_LISMO	Q5ne37 listeria mo
1425	794	2	166.5	5.3	Q2L8H1_LISMO	Q2l8h1 listeria mo
1426	794	2	166.5	5.3	Q2L8G9_LISMO	Q2l8g9 listeria mo
1427	794	2	166.5	5.3	Q2L8H5_LISMO	Q2l8h5 listeria mo
1428	794	2	166.5	5.3	Q2L8H2_LISMO	Q2l8h2 listeria mo
1429	794	2	166.5	5.3	Q2L8H7_LISMO	Q2l8h7 listeria mo
1430	794	2	166.5	5.3	Q2L8H4_LISMO	Q2l8h4 listeria mo
1431	794	2	166.5	5.3	Q2L8H3_LISMO	Q2l8h3 listeria mo
1432	797	2	166.5	5.3	Q4EJ83_LISMO	Q4ej83 listeria mo
1433	800	1	166.5	5.3	INLA_LISMF	Q723k6 listeria mo
1434	800	1	166.5	5.3	INLA_LISMO	P25146 listeria mo
1435	800	2	166.5	5.3	Q45GD5_LISMO	Q45gd5 listeria mo
1436	800	2	166.5	5.3	Q45GD6_LISMO	Q45gd6 listeria mo
1437	1012	2	166.5	5.3	Q95YI6_ASTPE	Q95yi6 asterina pe
1438	1115	2	166.5	5.3	Q652D9_ORYSA	Q652d9 oryza sativ
1439	1215	2	166.5	5.3	Q60PY2_CAEBR	Q60py2 caenorhabdi
1440	1270	2	166.5	5.3	Q7QHP7_ANOGA	Q7qhp7 anopheles g
1441	3204	2	166.5	5.3	Q95YI7_ASTPE	Q95yi7 asterina pe
1442	3204	2	166.5	5.3	Q6X248_9ALPH	Q6x248 bovine herp
1443	163	2	166	5.3	Q6E4F8_PETMA	Q6e4f8 petromyzon
1444	170	2	166	5.3	Q2VGK9_PETMA	Q2vgk9 petromyzon
1445	192	2	166	5.3	Q2VGK1_PETMA	Q2vgk1 petromyzon
1446	245	2	166	5.3	Q4KP01_LAMAP	Q4kp01 lampetra ap
1447	393	2	166	5.3	Q3UTG8_MOUSE	Q3utg8 mus musculu
1448	426	2	166	5.3	Q72TC3_LEPIC	Q72tc3 leptospira
1449	768	2	166	5.3	Q4SSE3_TETNG	Q4sse3 tetraodon n
1450	806	2	166	5.3	Q6P690_RAT	Q6p690 rattus norv
1451	835	1	166	5.3	TLR4_RAT	Q9qx05 rattus norv
1452	971	2	166	5.3	Q2A132_SALSA	Q2a132 salmo salar
1453	1030	2	166	5.3	TLR9_PIG	Q5i2m3 sus scrofa
1454	1030	2	166	5.3	Q865R8_PIG	Q865r8 sus scrofa
1455	1110	2	166	5.3	Q7G768_ORYSA	Q7g768 oryza sativ
1456	1221	2	166	5.3	Q9N523_CAEEL	Q9n523 caenorhabdi
1457	2139	2	166	5.3	Q4PDW0_USTMA	Q4pdw0 ustilago ma
1458	161	2	165.5	5.3	Q2VGK0_PETMA	Q2vgk0 petromyzon
1459	169	2	165.5	5.3	Q2VHG0_PETMA	Q2vhg0 petromyzon
1460	195	2	165.5	5.3	Q2VGU2_PETMA	Q2vgu2 petromyzon
1461	327	2	165.5	5.3	Q5RHE5_BRARE	Q5rhe5 brachydanio
1462	360	1	165.5	5.3	PGS2_BOVIN	P21793 bos taurus
1463	360	1	165.5	5.3	PGS2_CANFA	Q29393 canis famil
1464	360	2	165.5	5.3	Q3MHN1_BOVIN	Q3mhn1 bos taurus
1465	385	2	165.5	5.3	Q17EE7_AEDAE	Q17ee7 aedes aegyp
1466	526	2	165.5	5.3	Q7XJS3_ARATH	Q7xjs3 arabidopsis
1467	641	2	165.5	5.3	Q5H716_FUGRU	Q5h716 fugu rubrip
1468	1005	2	165.5	5.3	Q3L273_SPAAU	Q3l273 sparus aura
1469	1063	2	165.5	5.3	Q3L274_SPAAU	Q3l274 sparus aura
1470	1101	2	165.5	5.3	Q59H95_HUMAN	Q59h95 homo sapien
1471	1256	1	165.5	5.3	FLII_DROME	Q24020 drosophila
1472	1269	1	165.5	5.3	FLII_HUMAN	Q13045 homo sapien
1473	1269	2	165.5	5.3	Q5R4G9_PONPY	Q5r4g9 pongo pygma
1474	196	2	165	5.2	Q2VHO2_PETMA	Q2vho2 petromyzon
1475	283	2	165	5.2	Q4RX02_TETNG	Q4rx02 tetraodon n
1476	436	2	165	5.2	Q5R6F8_PONPY	Q5r6f8 pongo pygma
1477	780	2	165	5.2	Q299R7_DROPS	Q299r7 drosophila
1478	902	2	165	5.2	Q7RYP2_NEUCR	Q7ryp2 neurospora
1479	955	2	165	5.2	Q32NJO_XENLA	Q32nj0 xenopus lae
1480	994	2	165	5.2	Q9C637_ARATH	Q9c637 arabidopsis
1481	1135	2	165	5.2	Q7XS12_ORYSA	Q7xs12 oryza sativ
1482	1154	2	165	5.2	Q7QHH4_ANOGA	Q7qhh4 anopheles g
1483	171	2	164.5	5.2	Q2VH95_PETMA	Q2vh95 petromyzon
1484	185	2	164.5	5.2	Q2VGU7_PETMA	Q2vgu7 petromyzon
1485	235	2	164.5	5.2	Q4G1H9_EPTST	Q4g1h9 eptatretus
1486	437	2	164.5	5.2	Q1BQ30_9BURK	Q1bq30 burkholderi
1487	468	2	164.5	5.2	Q4LVE2_9BURK	Q4lve2 burkholderi
1488	582	1	164.5	5.2	SHOC2_HUMAN	Q9ug13 homo sapien
1489	582	2	164.5	5.2	Q5VZS9_HUMAN	Q5vzs9 homo sapien
1490	582	2	164.5	5.2	Q5RAV5_PONPY	Q5rav5 pongo pygma
1491	734	2	164.5	5.2	Q5R7N1_PONPY	Q5r7n1 pongo pygma

Right column table:

#	acc		val	5.2	code	species
1492	805	2	164.5	5.2	Q658W7_HUMAN	Q658w7 homo sapien
1493	810	2	164.5	5.2	Q2RBL3_ORYSA	Q2rbl3 oryza sativ
1494	819	2	164.5	5.2	Q659A9_HUMAN	Q659a9 homo sapien
1495	858	1	164.5	5.2	LRC8D_HUMAN	Q711w4 homo sapien
1496	958	2	164.5	5.2	Q28X54_DROPS	Q28x54 drosophila
1497	1421	2	164.5	5.2	Q2XXU4_DROYA	Q2xxu4 drosophila
1498	1426	2	164.5	5.2	Q2XXU5_DROYA	Q2xxu5 drosophila
1499	257	1	164	5.2	LRRC3_MOUSE	P59034 mus musculu
1500	257	2	164	5.2	Q54324_MOUSE	Q54324 mus musculu

ALIGNMENTS

RESULT 1

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VASN_HUMAN
ID   VASN_HUMAN         STANDARD;      PRT;     673 AA.
AC   Q6EMK4; Q6UXL4; Q6UXL5; Q96CX1;
DT   18-APR-2006, integrated into UniProtKB/Swiss-Prot.
DT   16-AUG-2004, sequence version 1.
DT   25-JUL-2006, entry version 17.
DE   Vasorin precursor (Protein Slit-like 2).
GN   Name=VASN; Synonyms=SLITL2; ORFNames=UNQ314/PRO357/PRO1282;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, INTERACTION WITH TGFB1; TGFB2
RP   AND TGFB3, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND
RP   GLYCOSYLATION.
RX   PubMed=15247411; DOI=10.1073/pnas.0404117101;
RA   Ikeda Y., Imai Y., Kumagai H., Nosaka T., Morikawa Y., Hisaoka T.,
RA   Manabe I., Maemura K., Nakaoka T., Imamura T., Miyazono K., Komuro I.,
RA   Nagai R., Kitamura T.;
RT   "Vasorin, a transforming growth factor beta-binding protein expressed
RT   in vascular smooth muscle cells, modulates the arterial response to
RT   injury in vivo.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:10732-10737(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ALA-384.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ALA-384.
RC   TISSUE=Lung, and Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   GLYCOSYLATION [LARGE SCALE ANALYSIS] AT ASN-117 AND ASN-273, AND MASS
RP   SPECTROMETRY.
RX   PubMed=16335952; DOI=10.1021/pro502065;
RA   Liu T., Qian W.-J., Gritsenko M.A., Camp D.G. II, Monroe M.E.,
RA   Moore R.J., Smith R.D.;
RT   "Human plasma N-glycoproteome analysis by immunoaffinity subtraction,
RT   hydrazide chemistry, and mass spectrometry.";
RL   J. Proteome Res. 4:2070-2080(2005).
CC   -!- FUNCTION: May act as an inhibitor of TGF-beta signaling.
CC   -!- SUBUNIT: Interacts with TGFB1, TGFB2 and TGFB3.
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC       protein (Probable). Secreted protein.
CC   -!- TISSUE SPECIFICITY: Expressed at highest levels in aorta, at
CC       intermediate levels in kidney and placenta and at lowest levels in
CC       brain, heart, liver, lung and skeletal muscle. Within the aorta,
CC       the strongest expression is found in the tunica media of the
CC       proximal ascending aorta, the descending thoracic aorta, the
CC       abdominal aorta and the coronary arteries. Within the kidney,
CC       expression is found in the interstitial cells.
CC   -!- PTM: N-glycosylated.
CC   -!- SIMILARITY: Contains 1 EGF-like domain.
CC   -!- SIMILARITY: Contains 1 fibronectin type-III domain.
CC   -!- SIMILARITY: Contains 11 LRR (leucine-rich) repeats.
CC
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR   EMBL; AY166584; AAO27704.1; -; mRNA.
DR   EMBL; AY358298; AAQ88665.1; -; mRNA.
DR   EMBL; AY358299; AAQ88666.1; -; mRNA.
DR   EMBL; BC013767; AAH13767.1; -; mRNA.
DR   EMBL; BC068575; AAH68575.1; -; mRNA.
DR   UniGene; Hs.372579; -.
DR   HSSP; Q9BZR6; 1P8T.
DR   Ensembl; ENSG00000168140; Homo sapiens.
DR   HGNC; HGNC:18517; VASN.
DR   MIM; 608843; gene.
DR   RZPD-ProtExp; IOH40553; -.
DR   InterPro; IPR006210; EGF.
DR   InterPro; IPR000742; EGF_3.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR013032; EGF_like_reg.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_C.
DR   InterPro; IPR000372; LRR_cys_N.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00008; EGF; 1.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00560; LRR_1; 8.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00369; LRR_TYP; 2.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS50026; EGF_3; 1.
DR   PROSITE; PS50853; FN3; 1.
KW   EGF-like domain; Glycoprotein; Leucine-rich repeat; Membrane;
KW   Polymorphism; Repeat; Signal; Transmembrane.
FT   SIGNAL        1     23       Potential.
FT   CHAIN        24    673       Vasorin.
FT                                /FTId=PRO_0000232630.
FT   TOPO_DOM     24    575       Extracellular (Potential).
FT   TRANSMEM    576    596       Potential.
FT   TOPO_DOM    597    673       Cytoplasmic (Potential).
FT   REPEAT       51     74       LRR 1.
FT   REPEAT       75     98       LRR 2.
FT   REPEAT      100    122       LRR 3.
FT   REPEAT      123    146       LRR 4.
FT   REPEAT      148    168       LRR 5.
FT   REPEAT      169    191       LRR 6.
FT   REPEAT      193    214       LRR 7.
FT   REPEAT      215    240       LRR 8.
FT   REPEAT      241    263       LRR 9.
FT   REPEAT      264    289       LRR 10.
FT   REPEAT      290    310       LRR 11.
FT   DOMAIN      405    442       EGF-like.
FT   DOMAIN      458    555       Fibronectin type-III.
FT   CARBOHYD    101    101       N-linked (GlcNAc...).          (Potential).
FT   CARBOHYD    117    117       N-linked (GlcNAc...).
FT   CARBOHYD    273    273       N-linked (GlcNAc...).          (Potential).
FT   CARBOHYD    500    500       N-linked (GlcNAc...).          (Potential).
FT   CARBOHYD    528    528       N-linked (GlcNAc...).
FT   DISULFID    409    420       By similarity.
FT   DISULFID    414    430       By similarity.
FT   DISULFID    432    441       By similarity.
FT   VARIANT     384    384       E -> A (in dbSNP:3810818).
FT                                /FTId=VAR_025991.
FT   CONFLICT     70     70       G -> S (in Ref. 2; AAQ88665).
FT   CONFLICT     91    165       Missing (in Ref. 2; AAQ88665).
SQ   SEQUENCE    673 AA;  71713 MW;  891B149652DEA286 CRC64;

Query Match            98.2%;  Score 3078.5;  DB 1;  Length 673;
Best Local Similarity  88.6%;  Pred. No. 1.8e-166;
Matches  596;  Conservative  0;  Mismatches  2;  Indels  75;  Gaps  1;

Qy     1  MCSRVPLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MCSRVPLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF   60

Qy    61  ENGITMLDASSFAGLPGLQLLDLSNQIAS-----------------------------   90
          ||||||||| ||||||||||||||| ||||
Db    61  ENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVQPLANLSNLDLTANRLHEITNETF  120

Qy    91  --------------------------------------------LRLPRLLLLDLSHNS  105
                                                      ||||||||||||||||
Db   121  RGLRLRERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNS  180

Qy   106  LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG  165
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG  240

Qy   166  LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPPRLRLLAAARNPF  225
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPPRLRLLAAARNPF  300

Qy   226  NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT  285
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT  360

Qy   286  TRPVVREPTALSSSSLAPTWLSPTAPATEAPSPPSTCLNGGTC                  345
          ||||||||||||||||||||||| ||||||||||||||||||
Db   361  TRPVVREPTALSSSSLAPTWLSPTEPATEAPSPPSTCLNGGTC                  420

Qy   346  HLGTRHHLACLCPEGTGLYCESQMGQGTRPSPTPVTRPPRSLTLGIEPVSPTSLRVGL   405
          |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   421  HLGTRHHLACLCPEGFGLYCESQMGQGTRPSPTPVTRPPRSLTLGIEPVSPTSLRVGL   480

Qy   406  QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP  465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP  540

Qy   466  GRVPEGEBACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR  525
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Db   541  GRVPEGEEACGEAHTPPAVHSNHAPVTQARRGNLPLLIAPALAAVLLAALAAVGAAYCVR  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   526  RGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPXATEGGGEALPSGSRCEVPLMGFPG  585

Db   601  RGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPXATEGGGEALPSGSECEVPLMGFPG  660

Qy   586  PGLQSPLHAKPYI  598
          |||||||||||||
Db   661  PGLQSPLHAKPYI  673
```

RESULT 2
VASN_MOUSE
ID VASN_MOUSE   STANDARD;   PRT;   673 AA.
AC Q9C2T5; Q8BJJ0; Q8R2G5;
DT 18-APR-2006, integrated into UniProtKB/Swiss-Prot.
DT 18-APR-2006, sequence version 2:
DT 13-JUN-2006, entry version 29.
DE Vasorin precursor (Protein Slit-like 2).
GN Name=Vasn; Synonyms=Slit2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=C57BL/6;
RA Schrewe H., Kutejova E.;
RT "Structure and expression analysis of the mouse Slit-like 2 (Slit2)
RT gene.";
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla D.A., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP DEVELOPMENTAL STAGE, AND INDUCTION.
RX PubMed=15247411; DOI=10.1073/pnas.0404117101;
RA Ikeda Y., Imai Y., Kumagai H., Nosaka T., Morikawa Y., Hisaoka T.,
RA Manabe I., Maemura K., Nakaoka T., Imamura T., Miyazono K., Komuro I.,
RA Nagai R., Kitamura T.;
RT "Vasorin, a transforming growth factor beta-binding protein expressed
RT in vascular smooth muscle cells, modulates the arterial response to
RT injury in vivo.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:10732-10737(2004).
CC -!- FUNCTION: May act as an inhibitor of TGF-beta signaling (By
CC   similarity).
CC -!- SUBUNIT: Interacts with TGFB1, TGFB2 and TGFB3 (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC   protein (Probable).
CC -!- DEVELOPMENTAL STAGE: Expression begins at E10.5 and increases as
CC   development progresses to E17.5. Expression rises in parallel with
CC   the differentiation of vascular smooth muscle cells (VSMCs) of the
CC   aorta.
CC -!- INDUCTION: Upon retinoic acid-induced differentiation of smooth
CC   muscle cells in vitro.
CC -!- PTM: N-glycosylated (By similarity).
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 fibronectin type-III domain.
CC -!- SIMILARITY: Contains 11 LRR (leucine-rich) repeats.
CC --
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC --
DR EMBL; AJ458938; CAD30331.1; -; mRNA.
DR EMBL; AK012169; BAB28075.1; -; mRNA.
DR EMBL; AK083684; BAC38992.1; -; mRNA.
DR EMBL; AK132325; BAB21105.1; -; mRNA.
DR EMBL; BC050274; AAH50274.1; -; mRNA.
DR UniGene; Mm.248337; -.
DR HSSP; P00740; 1EDM.
DR Ensembl; ENSMUSG00000039646; Mus musculus.
DR MGI; MGI:2177651; Vasn.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_C.

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Db  247 LAGNTRIAQIRPEDLAGLTALQELDVSNLSLQALPSDLSSLFPRLRLLAAARNPFNCLCP 306
Qy  231 LSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVV  :
Db  307 LSWFGPWVRENHVVLASPEETRCHFPPKNAGRLLLLDLDYADFGCPVTTTATVPTIRSTI 366
Qy  291 REPTALSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTR 350
Db  367 REPTLSTSSQAPTWPSLTEPTTQASTVLSTAPPTMRPAPQPQDCPASICLNGGSCRLGAR 426
Qy  351 HHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQ 410
Db  427 HHWECLCPEGFIGLYCESPVEQGMKPSSIPDTPRPPLLPLSIEPVSPTSLRVKLQRYLQ  486
Qy  411 GSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPE 470
Db  487 GNTVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSICVTPLGAGRTPE 546
Qy  471 GEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAM 530
Db  547 GEEACGEANTSQAVRSNHAPVTQAREGNLPLLIAPALAAVLLAVLAAAGAAYCVRRARA- 605
Qy  531 AAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQS  590
Db  606 TSTAQDKGQVGPGTGPLELEGVKAPLEPGSKATEGGGEALSGGPECEVPLMGYPGPSLQG 665
Qy  591 PLHAKPYI 598
Db  666 VLPAKHYI 673
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RESULT 3
VASN_XENTR
ID   VASN_XENTR              STANDARD;       PRT;   661 AA.
AC   Q6DF55;
DT   18-APR-2006, integrated into UniProtKB/Swiss-Prot.
DT   16-AUG-2004, sequence version 1.
DT   30-MAY-2006, entry version 15.
DE   Vasorin precursor.
GN   Name=vasn;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RG   NIH - Xenopus Gene Collection (XGC) project;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: May act as an inhibitor of TGF-beta signaling (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC       protein (Probable).
CC   -!- SIMILARITY: Contains 1 EGF-like domain.
CC   -!- SIMILARITY: Contains 1 fibronectin type-III domain.
CC   -!- SIMILARITY: Contains 11 LRR (leucine-rich) repeats.
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
DR   EMBL; BC076888; AAH76888.1; -; mRNA.
DR   UniGene; Str.8462; -.
DR   InterPro; IPR000372; LRR_cys_N.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00008; EGF; 1.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00560; LRR_1; 7.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00369; LRR_TYP; 7.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR006210; EGF.
DR   InterPro; IPR000742; EGF_3.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR013032; EGF_like_reg.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_C.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00008; EGF; 1.
DR   Pfam; PF00560; LRR_1; 8.
KW   EGF-like domain; Glycoprotein; Leucine-rich repeat; Membrane; Repeat;
KW   Signal; Transmembrane.
FT   SIGNAL        1     24
FT   CHAIN        25    673       Vasorin.
FT                                /FTId=PRO_0000232631.
FT   TOPO_DOM     25    576       Extracellular (Potential).
FT   TRANSMEM    577    597       Potential.
FT   TOPO_DOM    598    673       Cytoplasmic (Potential).
FT   REPEAT       52     75       LRR 1.
FT   REPEAT       76     99       LRR 2.
FT   REPEAT      101    123       LRR 3.
FT   REPEAT      124    147       LRR 4.
FT   REPEAT      149    169       LRR 5.
FT   REPEAT      170    192       LRR 6.
FT   REPEAT      194    215       LRR 7.
FT   REPEAT      216    241       LRR 8.
FT   REPEAT      242    264       LRR 9.
FT   REPEAT      265    287       LRR 10.
FT   REPEAT      289    311       LRR 11.
FT   DOMAIN      406    443       EGF-like.
FT   DOMAIN      459    556       Fibronectin type-III.
FT   CARBOHYD    102    102       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    118    118       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    274    274       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    501    501       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    529    529       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    555    555       N-linked (GlcNAc...) (Potential).
FT   DISULFID    410    421       By similarity.
FT   DISULFID    415    431       By similarity.
FT   DISULFID    433    442       By similarity.
FT   CONFLICT    225    225       S -> Y (in Ref. 2; BAB28075).
FT   CONFLICT    225    225       L -> H (in Ref. 2; BAC38992).
SQ   SEQUENCE   673 AA;  72261 MW;  AAB8DA82DA8E9D32 CRC64;

Query Match             79.4%;
Best Local Similarity   73.5%;
Matches   491;  Conservative   25;  Mismatches   25;  Indels   78;  Gaps    3;

Qy    6 PLLLPLLLLALGPGVQGCPSGCCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVPENGIT 65
Db    9 PLL--LLLVLGSGVQGCPSGCQCNQPQTVFCTARQGTTVPRDVPPDTVGLYIFENGIT   66
Qy   66 MLDASSFAGLPGLQLLDLSQNQIAS                                    90
Db   67 TLDVGCFAGLPGLQLLDLSQNQITSLPGGIFQPLVNLSNLDLTANKLHEISNETPRGLRR 126
Qy   91 ------LRLPRLLLLLDLSHNSLLALE                                 110
Db  127 LERLYLGKNRIRHIQPGAFDALDRLLELKLPDNELRVLPPLHLPRLLLLLDLSHNSIPALE 186
Qy  111 PGILDTANVEALRLAGLGLGQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLR 170
Db  187 AGILDTANVEALRLAGLGLGRQLDEGLFGRLNLNHDLDVSDNQLEHMPSVIQGLRGLTRLR 246
Qy  171 LAGNTRIAQIRPEDLAGLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAAARNPFNCVCP 230
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DR   PRINTS;  PR00019; LEURICHRPT.
DR   SMART;   SM00181; EGF; 1.
DR   SMART;   SM00369; LRR_TYP; 5.
DR   SMART;   SM00082; LRRCT; 1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS50026; EGF_3; 1.
DR   PROSITE; PS50853; FN3; FALSE_NEG.
KW   EGF-like domain; Glycoprotein; Leucine-rich repeat; Membrane; Repeat;
KW   Signal; Transmembrane.
FT   SIGNAL        1     19       Potential.
FT   CHAIN        20    661       Vasorin.
FT                                /FTId=PRO_0000232632.
FT   TOPO_DOM     20    563       Extracellular (Potential).
FT   TRANSMEM    564    584       Potential.
FT   TOPO_DOM    585    661       Cytoplasmic (Potential).
FT   REPEAT       49     72       LRR 1.
FT   REPEAT       73     96       LRR 2.
FT   REPEAT       98    120       LRR 3.
FT   REPEAT      121    144       LRR 4.
FT   REPEAT      146    166       LRR 5.
FT   REPEAT      167    189       LRR 6.
FT   REPEAT      191    212       LRR 7.
FT   REPEAT      213    236       LRR 8.
FT   REPEAT      237    258       LRR 9.
FT   REPEAT      259    281       LRR 10.
FT   REPEAT      283    306       LRR 11.
FT   DOMAIN      403    440       EGF-like.
FT   DOMAIN      455    543       Fibronectin type-III.
FT   CARBOHYD     99     99       N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD    518    518       N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD    561    561       N-linked (GlcNAc...)  (Potential).
FT   DISULFID    407    418       By similarity.
FT   DISULFID    412    428       By similarity.
FT   DISULFID    430    439       By similarity.
SQ   SEQUENCE   661 AA;  71958 MW;  A0AC47946BE8DBEA CRC64;

Query Match             38.7%;  Score 1213.5;  DB 1;  Length 661;
Best Local Similarity   41.3%;  Pred. No. 1.3e-60;
Matches  282;  Conservative  88;  Mismatches 158;  Indels 155;  Gaps  20;

Qy     8  LLPLLLLLALGPGV--QGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGIT  65
             ||  :||:|||         |::  || ||||||||||||||||||||||||||||||
Db     4  LLIWILLATAQQMITEGCPAGCQCNTPQTVFCLARKNSNFPRSVPPDTLNLYVFENGIS  63

Qy    66  MLDASSFAGLPGLQLLDLSQNQIASL------------------------------------  91
          ::  ||||| || ||||:|||
Db    64  SIEESSFIGLNGLHLLDLSHNQLSSLPGGVFRNLANLSNLDLTSNQLTEISADTFQGLSR  123

Qy    92  ------------------------------RLPRLLLDLSHNSLLALE  110
                                        ||| | :||:|||::|:|
Db   124  LERLYLNGNRIRSIHPEAFKGIESLLELKLSNNQLVTPPAFSLPHLLLLDLSYNAIPVIQ  183

Qy   111  PGILDTANVEALRLARLAGLGLQQLDEGLFSRLRNLHDLVSDNQLERVPPVIRGLTRLR  170
          :| ||: ||| |||  ||| |||| |||||||  |||| |||||:||||  |||||||||
Db   184  QGVFNAGNIESLRLRAGLGLKEVPEELLSGLKNLHELDLSDNQLDKVPP--GLHGLTKLN  240

Qy   171  LAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCP  230
           || |: ||||| | |||||| |||| ||| ::::|  ||||||||: |:|:||||||||
Db   241  IAGNVGFSQIQVDDLSNLPALQELDLSGLSLQTLPKGLFRSSKRLRAVSLAQNPFNCVCS  300

Qy   231  LSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLELDYADFGCPATTTTATVPTTRPVV  290
          | | ||| |:   |:||:  :||||||||| ||| :| ||::|||  |:::||  ||||
Db   301  LGWLSEWMRVSGVVLLRPDETRCHFPPKNAGKTLRQLRDSEYGCPA-PTTIQMPSTMPP-  358

Qy   291  REPTALSSSLAPTWLSPTAP--ATEAPSPPSTAPPTVGPVQPQD---------------CP  335
             ::    | : ||  |     ||:|::|:|||||| ::|||
Db   359  ------STTTGP-----PTTTKGHLQTEAPTTASTTTTTIPHQEQBEDTQPFQFDPBDTLCP  408

Qy   336  PSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSL---TLG  392
          |||||||||:  ||:|| ||:|||| |||||:||         |        : |:|  ::|:
Db   409  PQTCLNGGSCHLDPTGQLECECPPGFQGTYCET-----------GPVTPAVVTEMYIEQVK  458

Qy   409  ... GPVTPAVVTEMYIEQVK  458
```

Right column:

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Qy   393  IEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRP  452
          ||:| :|||:|||||| |::: |:|||||| ||| |||:|::|| |:||:| |:|||:||:|
Db   459  IIEVTVSSIRVDLQSYSQNKE-KLRAIRLTVRNLYGADRRPMIYKLPPTLPEYTVRALSS  517

Qy   453  NATYSVCVMPLGPGRVPEGEBEACGEAHT---PPAVHSNHAP-VTQAREGNLPLLIAPALA  508
          |:||::  | ||  |   |: :|  |:       :    |:|  |  | ||| |:| | ||
Db   518  NSSYWVCLGSQGEGG-PE-EDLCTETHTLGEPP----KHSPQVTQSQEGNLTLVLVPAVA  571

Qy   509  AVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGE  568
          | : || |:::|  ||:|    ::::        ::|:||||    |  :|||||||
Db   572  AGILLS-AAVAAACYARRR-----KGKGHSVEDGGPLEMDGVK------KGLDGKGE  617

Qy   569  AL--------PSGSECEVPLM  581
                        |:::| |||
Db   618  VKKLSEDPTGPKTGAESEEPLM  640
```

```
Query Match             31.0%;  Score 972.5;  DB 2;  Length 688;
Best Local Similarity   36.3%;  Pred. No. 6.6e-47;
Matches  239;  Conservative  77;  Mismatches 222;  Indels 121;  Gaps  15;

Qy     6  PLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGIT  65
```

RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Singapore local strain; TISSUE=Embryo;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC095341; AAH95341.1; -; mRNA.
DR   UniGene; Dr.45369; -.
DR   Ensembl; ENSDARG00000002890; Danio rerio.
DR   ZFIN; ZDB-GENE-050522-43; vasn.
DR   InterPro; IPR000742; EGF_3.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR013032; EGF_like_reg.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR000119; Hist_DNA_bd_bac.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_C.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00008; EGF; 1.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00560; LRR_1; 9.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM003369; LRR_TYP; 2.
DR   SMART; SM000082; LRRCT; 1.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS50026; EGF_3; 1.
DR   PROSITE; PS50853; FN3; 1.
DR   PROSITE; PS00045; HISTONE_LIKE; UNKNOWN_1.
SQ   SEQUENCE; 643 AA; 70201 MW; 964BE87924A7C642 CRC64;

Query Match   29.6%; Score 927.5; DB 2; Length 643;
Best Local Similarity   36.4%; Pred. No. 2.2e-44;
Matches 224; Conservative 77; Mismatches 201; Indels 113; Gaps 14;

Qy   46 VPRDVPPDTVGLYVFENGITMLDASSFAGLPGLQLDLSQNQIA-
               :|: ||||| :||||| : |||||||||| :||||||| ::
Db   1 MPRGLFSTGKQLYVFQNKINILQQQDFVELGELEMLDLSQNSLSEIPDGVFSPLSSLHNL   60

Qy   90 ---------------------------------S   90

Db   61 DLSSNYITHISKDSFIGLVNLERLYLYSNIIQNIHPAAFEGLENLLELKLQGNQISVLPA 120

Qy   91 LRLPRLLLLDLSHNSLLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSD 150
               |||||||||| :||:| ||||| | :. | ||| ||||||||| ||| |||||
Db   121 IQLPRLLHLDLSYNSIPPLVAQDLQTPHLESLKIAGLGLTSLDEELLGSLINLHVLDVSQ 180

Qy   151 NQLERVPPVIRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSG   210

Db   181 NQLVDIQPTLKSMGGLRNLNLTGNP-LGSLKHEDFQNLVNLLELDLSNLNLQGFPEGFPN 239

Qy   211 LFPRLRLLAAARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYA 270

Db   240 LFPKLEKLTAAENPFNCLCPLAWFPAWLKDVRVELLRTEETRCHFPPINSGKVLEKLEHK 299

Qy   271 DFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTPAATEAPSPPSTAPP----TVG 326

Db   300 DFGCPTTTIELTSAGTSSTTSKPTNSSTQSGTTHIVPPAPLSDISSADADNFPVYQTTAF 359

Qy   327 PVPQPQD------CPPSTCLNGGTCHLGTRHHLACLLCPEGFTGLYCESQMGGQGTRPSPT 379

Db   6 PLSHLILQLLCGCLSSRCPHDCTCLPSNNIFCVQRNLIYMPRGLPSTGKQLYVFQNKIN   65

Db   66 MLDASSFAGLPGLQLDLSQNQIA-   89

Db   66 ILQQQDFVELGELEMLDLSQNSLSEIPDGVFSPLSSLHNLDLSSNYITHISKDSFIGLVN 125

Qy   90 ---------------------SLRLPRLLLLDLSHNSLLALE   110

Db   126 LERLYLYSNIIQNIHPAAFEGLENLLELKLQGNQISVLPALRLPRLLLLDLSYNSIPPLV 185

Qy   111 PGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLTRLR   170

Db   186 AQDLQTPHLESLKIAGLGLTSLDEELLGSLINLHVLDVSQNQLVDIQPTLKSMGGLRNLN 245

Qy   171 LAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCP 230

Db   246 LTGNP-LGSLKHEDFQNLVNLLELDLSNLNLQGFPEGFPNLFPKLEKLTAAENPFNCLCP 304

Qy   231 LSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVV 290

Db   305 LAWFPAWLKDVRVELLRTEETRCHFPPINSGKVLEKLEHKDFGCPTTTIELTSAGTSSTT 364

Qy   291 REPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQP---------QD-------CP 335

Db   365 SKPKNSSTQLGTTHIVPPAP----PSDISSADADNFPVYQTTAFPSRIMEDSEGEGIMCP 420

Qy   336 PSTCLNGGTCHLGTRHHLACLLCPEGFTGLYCESQMGGQGTRPSPTP-------VTPRPPRS 388

Db   421 PNICLNGGTCIFKSNGVIVCLCPPSMSGNYCEIQ-NEAMLPPPSPRVSLETIATVQPN-- 477

Qy   389 LTLGIEPVSPTSLRVGLQRYLQGGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVT 448

Db   478 -TISSHHITSTSISLDLHRYIQ-TRPHIRGIRLTYSNLSGPDRRPIQLSVPPSYPEYTLR 535

Qy   449 QLRPNATYSVCVMPLGPGPRVPEGEEACGEAHT---PPAVHSNHAPVTQAREGNLPLLIAP 505

Db   536 GLQPNSTYSVCASPLGE-PVHASVSACMEARTAGIPPSSHEPSVDRTEPSSSLTPIVV-- 592

Qy   506 ALAAVLLAALAAVGAAYCVRRGRAMAAAAAQDKGQVGPGAGPLELEGVKVPLEPG---PK 561

Db   593 AVAVMWVAIIAT-VVVISRRRRPKAPVDMDLHE----TSPLEMEGVKTNPENGLTHPK 646

RESULT 5
Q503G2_BRARE
ID   Q503G2_BRARE   PRELIMINARY;   PRT;   643 AA.
AC   Q503G2;
DT   07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT   07-JUN-2005, sequence version 1.
DT   13-JUN-2006, entry version 10.
DE   Slit-like 2.
GN   Name=vasn;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Singapore local strain; TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

```
Db    360  PSRIMEDSEGEGIMCPPNICLNGGTCIFKSNGVIVCLCPPSMSGLYCEIQ-NEAMLPPPS  418
Qy    380  P-------VTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKR  432
                    |  :|        ::  ||  :  ||:|  :  :|||  ||||||
Db    419  PRVSLETIATVQPN---TISSHHITSTSISLDLHRYIQ-TRPHIRGIRLTYSNLSGPDRR  474
Qy    433  LVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT---PPAVHSNHA  489
                 :|:|  ::||:    ||||  |  :||:|| :  :||||
Db    475  PLQLSVPPSYPEYTLRGLQPNSTYSVCASPLGE-PVHASVSACMEARTAGIPPSSHEPSV  533
Qy    490  PVTQAREGNLPLLIAPALAAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGPGAGPLEL  549
                ||  :||  :|:|:  :|  |:  ||:|
Db    534  DRTEPSSSLTPIVV--AVAVMVVAIIAT-VVVISRRRRPKAPVDMDLHE----TSPLEM  586
Qy    550  EGVKVPLEPG---PK  561
                |||| ||   ||
Db    587  EGVKTNPENGLTHPK  601


RESULT 6
Q4SQ68_TETNG
ID    Q4SQ68_TETNG     PRELIMINARY;    PRT;   962 AA.
AC    Q4SQ68;
DT    19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT    19-JUL-2005, sequence version 1.
DT    02-MAY-2006, entry version 7.
DE    Chromosome 19 SCAF14535, whole genome shotgun sequence.
GN    ORFNames=GSTENG00014497001;
OS    Tetraodon nigroviridis (Green puffer).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC    Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC    Tetraodontoidea; Tetraodontidae; Tetraodon.
OX    NCBI_TaxID=99883;
RN    [1]
RP    NUCLEOTIDE SEQUENCE.
RX    PubMed=15496914; DOI=10.1038/nature03025;
RA    Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA    Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA    Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA    Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA    Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA    Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA    Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA    Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA    Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA    Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA    Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA    Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT    "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT    the early vertebrate proto-karyotype.";
RL    Nature 431:946-957(2004).
RN    [2]
RP    NUCLEOTIDE SEQUENCE.
RG    Genoscope; Whitehead Institute Centre for Genome Research;
RL    Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC    -!- CAUTION: The sequence shown here is derived from an
CC        EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC        preliminary data.
CC    --------------------------------------------------------------------
CC    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC    Distributed under the Creative Commons Attribution-NoDerivs License
CC    --------------------------------------------------------------------
DR    EMBL; CAAE01014535; CAP97214.1; -; Genomic_DNA.
DR    GO; GO:0005634; C:nucleus; IEA.
DR    GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR    InterPro; IPR000742; EGF_3.
DR    InterPro; IPR006209; EGF_like.
DR    InterPro; IPR013032; EGF_like_reg.
DR    InterPro; IPR003961; FN_III.
DR    InterPro; IPR008957; FN_III-like.
DR    InterPro; IPR001611; LRR.
DR    InterPro; IPR000483; LRR_C.
```

```
DR    InterPro; IPR003591; LRR_typ.
DR    InterPro; IPR005033; YEATS.
DR    Pfam; PF00008; EGF; 1.
DR    Pfam; PF05560; LRR_1; 8.
DR    Pfam; PF03366; YEATS; 1.
DR    PRINTS; PR00019; LEURICHRPT.
DR    SMART; SM00369; LRR_TYP; 2.
DR    SMART; SM00082; LRRCT; 1.
DR    PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR    PROSITE; PS50026; EGF_3; 1.
DR    PROSITE; PS50853; FN3; 1.
DR    PROSITE; PS51037; YEATS; 1.
SQ    SEQUENCE   962 AA;  106856 MW;  3EC2C9402AC80BF6 CRC64;

Query Match             29.2%;  Score 914.5;  DB 2;  Length 962;
Best Local Similarity   38.0%;  Pred. No. 1.8e-43;
Matches  222; Conservative  77; Mismatches 190; Indels  95; Gaps  18;

Qy     57  LYVFENGITMLDASSFAGLPGLQLLDLSQNQIA---SLRLPRLLLLDLSHNSLLALEPGI  113
               |::             |:   |::|||||         ::|| |:| ::||||||||
Db    388  LYLHGNLIQSIHABAFEGLEMLLELKLQGNQLSSLPSLRFPRLLLLLDLSNNNIPSLGPSD  447

Qy    114  LDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLRVPPVIR--GLRGLTRLRL  171
               :  |: ||  | | || ||  |||: |:  |  | |:    :  |  ::    :|
Db    448  FQTPHLEALKIVSLGMSLGDELIASMRNLHELDISMNQLTEVPLALKQDSLKGLIKLSL  507

Qy    172  AGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPL  231
               ||  |             ||||||  |||  |::|||| |:||||| :|| ||| ||
Db    508  AGNP-LGDLRVEDFEKLTSLQELDLGLNLQGFSPSPSLEMPRLTQLTAAENPFNCLCPL  566

Qy    232  SWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVR  291
               ::||            | ||| |           :| ||  |     | ::   :
Db    567  AWFPVWLKEKKVNLRRPEETRCHFPLVNAGKKLSALETRDFGCPLTT---TLP-----IG  618

Qy    292  EPTALSSSLAPTWLSPTAPATEAPSPPSTAP---PTVGPVPQPQD----  333
               |                 ::               ||::|| |
Db    619  SPTGSTPSIPVSTTPKMTYTNAIPPPPPPSEEILPSKTYPLPPEPTFSPSSTSGEVE  678

Qy    334  ---CPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVVTPRPPR--  387
                     :|||||||   :|||| :   |||  |:|| :      |       ::|||
Db    679  SHICPANICLNGGTCHFDPMGQLSCICLSGTSGLYCEN---------VDIVPDPPKHPV  728

Qy    388  ---SLTLGIEP-------VSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLV  434
                   :|:|||        |||:|||||||||||||||||||||||||||||||
Db    729  TEATLAASSVPVQNDAISSRQVTSTSLLLDLQRFIE-TRPHIRGIRLLYRNLSGPDRRPM  787

Qy    435  TLRLPASLAEYTVTQLRPNATYSVCVMPLGP-----GRVPEGEEACGEAHT-------  480
               |||||||||||||||||||||:||||||||      ||:||||| |||||
Db    788  ILSVPASYPEYTLRGLKPNCTYSVCASPLGERVSLRANSSVDTG--SCTEARTEGILMTS  845

Qy    481  PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV  540
               |||:|  |   ||:||:|:|:||:|:|||||:|||||||||||||||| |||||||||
Db    846  SSATAPTPGPMT------FTLILAVSALALVLGVSLVAGTVICVRK-RREAKAGMELEMA  898

Qy    541  GPGAGPLELEGVKVPLEPGPKATEGGGEALPSG----SECEVPL  580
               |||| || ||||:|||||||||             :||| ||
Db    899  PADSDPMELDGMKLGLENGANGT-----LPHKQAQINRCHTPL  936


RESULT 7
LRC24_HUMAN
ID    LRC24_HUMAN     STANDARD;    PRT;   513 AA.
AC    Q5OLG9;
DT    04-APR-2006, integrated into UniProtKB/Swiss-Prot.
DT    07-JUN-2005, sequence version 1.
DT    30-MAY-2006, entry version 10.
DE    Leucine-rich repeat-containing protein 24 precursor.
GN    Name=LRRC24;
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC    Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
```

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RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Brain;
RA   Shimizu N., Asakawa S., Shimizu A., Yamazaki S., Ishikawa S.K.;
RT   "Novel gene containing leucine rich repeat on human chromosome 8.";
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass membrane protein
CC       (Potential).
CC   -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC       domain.
CC   -!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.
CC   --------------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   --------------------------------------------------------------------------
DR   EMBL; AB178281; BAD97811.1; -; mRNA.
DR   EMBL; BC111067; AAI11068.1; -; mRNA.
DR   UniGene; Hs.591399; -.
DR   Ensembl; ENSG00000188270; Homo sapiens.
DR   HGNC; HGNC:28947; LRRC24.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR013098; Ig_I-set.
DR   InterPro; IPR003599; Ig_sub.
DR   InterPro; IPR003598; Ig_sub2.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_C.
DR   InterPro; IPR000372; LRR_cys_N.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF07679; I-set; 1.
DR   Pfam; PF00560; LRR_1; 5.
DR   Pfam; PF01463; LRRCT; 1.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00369; LRR_TYP; 3.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Membrane;
KW   Repeat; Signal; Transmembrane.
FT   SIGNAL        1     20       Potential.
FT   CHAIN        21    513       Leucine-rich repeat-containing protein
FT                                24.
FT                                /FTId=PRO_0000231596.
FT   TRANSMEM    406    426       Potential.
FT   REPEAT       49     72       LRR 1.
FT   REPEAT       73     96       LRR 2.
FT   REPEAT       98    120       LRR 3.
FT   REPEAT      122    144       LRR 4.
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FT   REPEAT      145    168       LRR 5.
FT   REPEAT      170    192       LRR 6.
FT   REPEAT      244    265       LRR 7.
FT   DOMAIN      260    361       Ig-like C2-type.
FT   COMPBIAS    375    378       Poly-Pro.
FT   COMPBIAS    427    432       Poly-Arg.
FT   CARBOHYD    334    334       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    334    334       N-linked (GlcNAc...) (Potential).
FT   DISULFID    281    363       By similarity.
SQ   SEQUENCE    513 AA;  55199 MW;  3770FA80D979C1DE CRC64;

Query Match             11.8%;  Score 368.5;  DB 1;  Length 513;
Best Local Similarity   26.4%;  Pred. No. 9.3e-13;
Matches  170;  Conservative   63;  Mismatches  217;  Indels  195;  Gaps   28;

Qy     1  MCSRVPLLIPLLLLALGPGVQCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF   60
          ||||||||  | | |||||| |||||   ||| :|:|:|||  |   : |||  ||||
Db     1  MALRAPALLPLLLLL-LPLRAAGCPAACRC-YSATVECGALRLRVVPLGIPPGTQTLFLQ   58

Qy    61  ENGITMLDASSFAGLPGLQLLDSQNQIASRL------PRLLLDLSHNSLLALEPG-I  113
          :|| |  ||:|| | ||| :|   | ||||        :|| |  || | :|  |
Db    59  DNNIARLEPGALAPLAALRRLYIHNNSLRALEAGAFRAQPRLLELALTSNRLRGLRSGAF  118

Qy   114  LDTANVEALRLRALGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAG  173
          : | ||||||||||| |  |||  | ::|:| |:||: ||:|   | :|:  || || |
Db   119  VGLAQLRVLYLYAGNQLARLLDFTFLHIPRLQELHLQENSIE-------------------  159

Qy   174  NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSW  233
          :   ||  : ||| | |||| || | :   : | |  |:      ::|  |:||:|
Db   160  ----LLEDQALAGLSSLALLDLSRNQLGTISREALQPLASLQVLRLTENPWRCDCALHW  214

Qy   234  FGPWVRESHVTLASPEETR--CHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVR  291
          | |  : |:|:|  |: :    : |    || : | : || | |  |  |  :||  |
Db   215  LGAWIKEGGQRLLTSRDRKIMCAEPPRLALQSLLDVSHSSLIC--------IPPSVHV-  264

Qy   292  EPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPVQPQDCPP--STCLNGGTCHLGT  349
          :|:::| |:||     ||        : ||  |         |:       ::|||||||
Db   265  QPLELTANLGED-LRVACQASGYPQP---LVTWRKVPQPREGRPRAQAQLEGLL--LGL  317

Qy   350  RHHLACLCPEGF---------------TGLY-CESQMGQG----------TRPSP-TPVTPRP  385
          ::|||:|||        | ||  :|
Db   318  GGHSASDTGSGMLFLSNITLAHAGKYECEASNAGGAARVPFRLLVNASRQQPQQPAQPPP  377

Qy   386  PRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY  445
          |||  | | |
Db   378  PAARPAGSEP--------------------------------------------------  387

Qy   446  TVTQLRPNATYSVCVMPLGPGRVPEGEBEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAP  505
          | || ||| :|      |  || |||:|||:||||||:|||:||||:||   ||||||||
Db   388  -----RPEAG-SMAFRALG--------------------------VATQT----AIAA  409

Qy   506  ALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGPGA--------GP---LELEGVK-  553
          :|:|:| ||  :     :  | |   :           | :|:    ||     |:||:
Db   410  AIALLALTALLLV-AMICRRRRRKKA----RGPPGEGALFVNDYLDGPCTFAQLEBLRD  464

Qy   554  --------VPLEPGPKATEGGGGEALPSGSECEVPLMGFPGPGLQSP  591
          |||  |:| |||| ||| ||| :| ::| :|     | ||  |
Db   465  ERGHEMFVINRSKPLFABGPAEA---PADCG-PAQG-AGPGLRVP  504
```

```
RESULT 8
LRFN4_HUMAN
ID   LRFN4_HUMAN             STANDARD;      PRT;    635 AA.
AC   Q6PJG9; Q9BWJ0;
DT   29-MAR-2005, integrated into UniProtKB/Swiss-Prot.
DT   05-JUL-2004, sequence version 1.
DT   13-JUN-2006, entry version 27.
DE   Leucine-rich repeat and fibronectin type-III domain-containing protein
DE   4 precursor.
GN   Name=LRFN4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
```

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OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Eye, and Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC       protein (Potential).
CC   -!- SIMILARITY: Contains 1 fibronectin type-III domain.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   -!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.
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DR   EMBL; BC00207; AAH00207.2; -; mRNA.
DR   EMBL; BC015581; AAH15581.2; -; mRNA.
DR   UniGene; Hs.209979; -.
DR   Ensembl; ENSG00000173621; Homo sapiens.
DR   HGNC; HGNC:28456; LRFN4.
DR   LinkHub; Q6PJG9; -.
DR   RZPD-ProtExp; IOH23019; -.
DR   RZPD-ProtExp; V0090; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007291; Ig-like.
DR   InterPro; IPR013098; Ig_I-set.
DR   InterPro; IPR003599; Ig_sub.
DR   InterPro; IPR003598; Ig_sub2.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_C.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF07679; I-set; 1.
DR   Pfam; PF00560; LRR_1; 5.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00369; LRR_TYP; 2.
DR   SMART; SM00082; LRRCT; 1.
DR   PROSITE; PS50853; FN3; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Membrane;
KW   Polymorphism; Repeat; Signal; Transmembrane.
FT   SIGNAL        1     16       Potential.
FT   CHAIN        17    635       Leucine-rich repeat and fibronectin type-
FT                                III domain-containing protein 4.
FT                                /FTId=PRO_0000014843.
FT   TOPO_DOM     17    518       Extracellular (Potential).
FT   TRANSMEM    519    539       Potential.
FT   TOPO_DOM    540    635       Cytoplasmic (Potential).
FT   REPEAT       46     70       LRR 1.
FT   REPEAT       71     94       LRR 2.
FT   REPEAT       95    118       LRR 3.
FT   REPEAT      120    142       LRR 4.
FT   REPEAT      144    167       LRR 5.
FT   REPEAT      168    191       LRR 6.
FT   REPEAT      193    216       LRR 7.
FT   DOMAIN      281    367       Ig-like.
FT   DOMAIN      407    492       Fibronectin type-III.
FT   CARBOHYD     25     25       N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD     70     70       N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD    324    324       N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD    333    333       N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD    376    376       N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD    440    440       N-linked (GlcNAc...)  (Potential).
FT   DISULFID    302    351       By similarity.
FT   VARIANT     340    340       V -> A (in dbSNP:3741194).
FT                                /FTId=VAR_024499.
SQ   SEQUENCE   635 AA;  66860 MW;  13B6645A17A92EE CRC64;

Query Match             11.5%;  Score 359.5;  DB 1;  Length 635;
Best Local Similarity   27.6%;  Pred. No. 3.8e-12;
Matches  169;  Conservative   61;  Mismatches  281;  Indels  101;  Gaps   23;

Qy      8 LLPLLLLLALGPGVQGCPSGCQC--SQPQTVFCTARQGTVPRDVPPDTVGLYVFENGI 64
          ||||||||:.||. | | ||| |  :: |||| ||:|.| | .:|||||||:| |||
Db      1 MAPPLLLLLASGAAACPLPCVCQNLSESLSTLCAHRGLLFVPPNVDRRTVELRLADNFI 60

Qy     65 TMLDASSPAGLPGLQLDLSQNQIASL------RLPRLLLDLSHNSLLALEPGIL-DTA 117
          . |.  .|| . || ||| |: | ||      ||| ||.||| |.| : . |.| .
Db     61 QALGPPDFRNMTGLVDLTLSRNAITRIGARAFGDLESLRSLHLDGNRLVELGTGSLRGPV 120

Qy    118 NVEALRLAGLGLQQLDEGLFSR-LRNLHDLLDVSDNQLERVP-PVIRGLRGLTRLRLAGNT 175
          |.: | |:|. |.: . ||    |.|||||||:|:|||| || | | |: | | | |.|
Db    121 NLQHLILSGNQLGRIAPGAFDDFLESLEDLDLSYNNLRQVPWAGIGAMPALHTLNLDHNL 180

Qy    176 RIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLR--------LLAAARNPFN 226
          .|  | |. .| | .:.|||:||| | |:| . ::  |: |        :|:  .|| |
Db    181 -IDALPPGAFAQLGQLSRLDLTSNRLATLAPD--PLFSRGRDAEASPAPLVLSFSGNPLH 237

Qy    227 CVCPLSWFGPWVRESHVTLASPEETR-CHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
          | | |.|    ||.  | ||.     | :  . : || :|:|||.|: |.
Db    238 CNCELLWLR-------RLARPDDLETCASPPGLAGRYFWAVPEGEFSC------------ 278

Qy    286 TRPVVREPTALSSSLAPTWLSPTAPAT---EAPSPPSTAPPTVGPVPVPQ-------PQDCPP 336
          |.|: .  |. :.  .:|   :.:|.|   :|   ..    . || |:
Db    279 ------EPPLIARHTQRLWVLEGQRATLRCRALGDPAPTMHWVGPDDRLVGNSSRARAFP 332

Qy    337 STCLNGGTCHLGTRHHLACLC--PEGFTGLYCE------------SQMGQGTRPSPTVPTPR 384
          . | :|.|  .  .:: || :  |.| ||| |:             .. .|  |.| | | |
Db    333 NGTLEIGVTGAGDAGGYTCIATNPAGEATARVELRVLALPHGGNSSAEGGRPGPSDIAAS 392

Qy    385 PPRSL---TLGIEP---VSPTSLRVGLQRYLQGSSVQ-LRSLRLTYRNLSGPDKRLVTL 436
          . |..   ||. |    |: ||:.  .. : | ...: ||  : | .||.| | :.: |
Db    393 ARTAAEGEGTLESEPAVQVTEVTATSGLVSWGPGRPADPVWMFQIQYN--SSEDETLIYR 450

Qy    437 RLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEA-----CGEAHTPPAVHSNHAPV 491
          .:|||. .: : |:.| | | : .:.|. .  |.. :|     | .| |. |:.. | |
Db    451 IVPASSHFLLKHLVPGADYDLCLLALSPAAGPSDLTATRLLGCAHFSTLPASPLCHALQ 510

Qy    492 TQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGPGAGPLELEG 551
          . .  | | |:::| || |:|.||  | ||:  || |..      | ||  | |: |
Db    511 AHVLGGTLTV----AVGGVLVAALLVFTVALLV-RGRG---------AGNGRLPLKLSH 555

Qy    552 VKVPLEPGPKAT 563
          |:. :  || .|
Db    556 VQSQTNGGPSPT 567


RESULT 9
LRFN4_MOUSE
ID   LRFN4_MOUSE STANDARD;  PRT;  636 AA.
AC   Q80XU8; Q3TQG8; Q8K3C4;
DT   29-MAR-2005, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-2003, sequence version 1.
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DT   13-JUN-2006, entry version 30.
DE   Leucine-rich repeat and fibronectin type-III domain-containing protein
DE   4 precursor.
GN   Name=Lrfn4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=C57BL/6J; TISSUE=Adipose tissue, and Head;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam H., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki Y., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Eye, and Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC       protein (Potential).
CC   -!- SIMILARITY: Contains 1 fibronectin type-III domain.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   -!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.
CC   ------------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ------------------------------------------------------------------------
DR   EMBL; AK081560; BAC38259.1; -; mRNA.
DR   EMBL; AK163603; BAE37415.1; -; mRNA.
DR   EMBL; BC023036; AAH23036.1; -; mRNA.
DR   EMBL; BC023156; AAH23156.1; -; mRNA.
DR   UniGene; Mm.329675; -.
DR   HSSP; Q9BZR6; 1P8T.
DR   Ensembl; ENSMUSG00000045045; Mus musculus.
DR   MGI; MGI:2385612; Lrfn4.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR013098; Ig_I-set.
DR   InterPro; IPR003599; Ig_sub.
DR   InterPro; IPR003598; Ig_sub2.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_C.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF07679; I-set; 1.
DR   Pfam; PF00560; LRR_1; 5.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00369; LRR_TYP; 2.
DR   SMART; SM00082; LRRCT; 1.
DR   PROSITE; PS50853; FN3; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Membrane;
KW   Repeat; Signal; Transmembrane.
FT   SIGNAL        1     16       Potential.
FT   CHAIN        17    636       Leucine-rich repeat and fibronectin type-
FT                                III domain-containing protein 4.
FT                                /FTId=PRO_0000014844.
FT   TOPO_DOM     17    518       Extracellular (Potential).
FT   TRANSMEM    519    539       Potential.
FT   TOPO_DOM    540    636       Cytoplasmic (Potential).
FT   REPEAT       46     70       LRR 1.
FT   REPEAT       71     94       LRR 2.
FT   REPEAT       95    118       LRR 3.
FT   REPEAT      120    142       LRR 4.
FT   REPEAT      144    167       LRR 5.
FT   REPEAT      168    191       LRR 6.
FT   REPEAT      193    216       LRR 7.
FT   DOMAIN      281    367       Ig-like.
FT   DOMAIN      407    492       Fibronectin type-III.
FT   CARBOHYD     25     25       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     70     70       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    324    324       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    333    333       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    376    376       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    440    440       N-linked (GlcNAc...) (Potential).
FT   DISULFID    302    351       By similarity.
FT   CONFLICT    503    503       T -> N (in Ref. 2; AAH23156).
SQ   SEQUENCE   636 AA;  67252 MW;  1EB86E96CB88BA91 CRC64;
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Query Match   11.2%; Score 351; DB 1; Length 636;
Best Local Similarity   27.2%; Pred. No. 1.2e-11;
Matches 170; Conservative 62; Mismatches 276; Indels 116; Gaps 25;

Qy   8 LLPLLLLALGSPGVQGCPSGGCQC---SQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGI 64

Db   1 MAPPLLLLLASGAAACPLPCVCQNLSESLSTLCAHRGLLFVPPNVDRRTVELRLADNFI 60

Qy   65 TMLDASSFAGLPGLQLLDLSQNQIASL------RLPRLLLLDLSHNSLLAL-EPGILDTA 117
            |::|||: ||:|| |:| :|| : ||:||||||||||||:| ::|||||
Db   61 QALGPPDFRNMTGLVDLTLSRNAITRIGARSFGDLESLRSLHLDGNRLVELGSSSLRGPV 120

Qy 118 NVEALRLAGLGLQQLDEGLFSR-LRNLHDLDVSDNQLERVP-PVIRGLRGLTRLRLAGNT 175
             |::.|||: ||:|: ::| |||| | |||:||:| : |||||:|:|| |::
Db 121 NLQHLILSGNQLGRIAPGAFDDFLDSLEDLDVSYNNLRQVPWAGIGSMPALHTLNLDHNL 180

Qy 176 RIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLR--------LLAAARNPFN 226
            ||:   ::|||||||||:|: |||:| :| : | |::   :|
Db 181 -IDALPPGVFAQLSQLSRLDLTSNRLATLAPD--PLFSRGRDAEASPSPLVLSFSGNPLH 237

Qy 227 CVCPLSWFGPWVRESHVTLASPEETR-CHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
            |||| | :   : :| :||: : |: |: |||| | |
Db 238 -RLARPDDLETCASPPTLAGRYFWAVPEGEFSC-------------------------- 278

Qy 286 TRPVVREPTALSSSLAPTWLSPTAPAT---EAPSPPSTAPPTVGPVPQPQD-------- 333
                 :   : |: | ||:| | :||||:| | |
Db 279 ------EPPLIARHTQRLWVLEGQRATLRCRALGDPVPTMHWVG----PDDRLVGNSSRA 328

Qy 334 -CPPSTCLNGGTCHLGTRHHLACLC--PEGFTGLYCESQM----------GQGTRPSPTP 380
            |||| ||||| ||| :||||| || | ||| ||:| ||| | | |
Db 329 WAFPNGTLEIGVTGAGDAGAYTCIATNPAGEATARVELRVLALPHGGNTSAEGGRPGPSD 388

Qy 381 VTPRPPRSL----TLGIEP--VSPTSLRVGLQRYLQGSSVQ-LRSLRLTYRNLSGPDKR 432
             ::| |||:| : || ||:|||:| |::: : || | ||:|||:|
Db 389 IAASARTAAEGEGTLESEPAVQVTEVTATSGLVSWGLGRPADPVWMFQIQYN--SSEDET 446

Qy 433 LVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEA------CGEAHTPPAVHSN 487
            |: |:|||::| | | |: ||:|| |::||| |||||| ||||| || |
Db 447 LIYRIVPASSHHFLLKGHLVPGADYDLCLLALSPAAGPSDLTATRLLGCAHFSTLPATPLC 506

Qy 488 HAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGPGAGPL 547
            || | ||| :|| ::| ||:|:||| ||||| |||| | ||:|
Db 507 HALQAHVLGGTLTV---AVGGVLVAALLVFTVALLV-RGRG-----------AGNGRLPL 551

Qy 548 ELEGVKVPLEPGPKATEGGGEALP 571
             :| :| || ||
Db 552 KLSHVQ------SQTNGGTSPMP 568

RESULT 10
Q460G5_MOUSE
ID   Q460G5_MOUSE   PRELIMINARY;   PRT;   636 AA.
AC   Q460G5;
DT   13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2005, sequence version 1.
DT   27-JUN-2006, entry version 8.
DE   Synaptic adhesion-like molecule 3.
GN   Name=Lrfn4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BALB/c;
RA   Wang C.-Y., Wenthold R.J.;
RT   "Synaptic Adhesion-Like Molecules, a Novel Family of Proteins
RT   Interacting with NMDA Receptor and MAGUKs.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---
DR   EMBL; DQ078786; AAZ23615.1; -; mRNA.
DR   MGI; MGI:2385612; Lrfn4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR013098; Ig_I-set.
DR   InterPro; IPR003599; Ig_sub.
DR   InterPro; IPR003598; Ig_sub2.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_C.
DR   InterPro; IPR003591; LRR_typ.
     Pfam; PF00041; fn3; 1.
     Pfam; PF07679; I-set; 1.
     Pfam; PF00560; LRR_1; 5.
     PRINTS; PR00019; LEURICHRPT.
     SMART; SM00409; IG; 1.
     SMART; SM00408; IGc2; 1.
     SMART; SM00369; LRR_TYP; 2.
     SMART; SM00082; LRRCT; 1.
     PROSITE; PS50853; FN3; 1.
     PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   636 AA; 67265 MW; 9C86E8A39B1A884 CRC64;

Query Match   11.1%; Score 348; DB 2; Length 636;
Best Local Similarity   27.2%; Pred. No. 1.7e-11;
Matches 170; Conservative 62; Mismatches 276; Indels 25; Gaps 25;

Qy   8 LLPLLLLLALGPGVQGCPSGCQC--SQPQTVFCTARQGTVPRDVPPDTVGLYVENGI 64
            :||||||| ||| || | | | ::| :|| ||:| :|| || | ||| :|:
Db   1 MAPPLLLLLASGAAACPLPCVCQNLSESLSTLCAHRGLLFVPPNVDRRTVELRLADNFI 60

Qy   65 TMLDASSFAGLPGLQLLDLSQNQIASL------RLPRLLLLDLSHNSLLAL-EPGILDTA 117
            |::|||: ||:|| |:| :|| : ||:||||||||||||:| ::|||||
Db   61 QALGPPDFRNMTGLVDLTLSRNAITRIGARSFGDLESLRSLHLDGNRLVELGSSSLRGPV 120

Qy 118 NVEALRLAGLGLQQLDEGLFSR-LRNLHDLDVSDNQLERVP-PVIRGLRGLTRLRLAGNT 175
             |::.|||: ||:|: ::| |||| | |||:||:| : |||||:|:|| |::
Db 121 NLQHLILSGNQLGRIAPGAFDDFLDSLEDLDVSYNNLRQVPWAGIGSMPALHTLNLDHNL 180

Qy 176 RIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLR--------LLAAARNPFN 226
            ||:   ::|||||||||:|: |||:| :| : | |::   :|
Db 181 -IDALPPGVFAQLSQLSRLDLTSNRLATLAPD--PLFSRGRDAEASPSPLVLSFSGNPLH 237

Qy 227 CVCPLSWFGPWVRESHVTLASPEETR-CHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
            |||| | :   : :| :||: : |: |: |||| | |
Db 238 -RLARPDDLETCASPPTLAGRYFWAVPEGEFSC-------------------------- 278

Qy 286 TRPVVREPTALSSSLAPTWLSPTAPAT---EAPSPPSTAPPTVGPVPQPQD-------- 333
                 :   : |: | ||:| | :||||:| | |
Db 279 ------EPPLIARHTQRLWVLEGQRATLRCRALGDPVPTMHWVG----PDDRLVGNSSRA 328

Qy 334 -CPPSTCLNGGTCHLGTRHHLACLC--PEGFTGLYCESQM----------GQGTRPSPTP 380
            |||| ||||| ||| :||||| || | ||| ||:| ||| | | |
Db 329 WAFPNGTLEIGVTGAGDAGAYTCIATNPAGEATARVELRVLALPHGGNTSAEGGRPGPSD 388

Qy 381 VTPRPPRSL----TLGIEP--VSPTSLRVGLQRYLQGSSVQ-LRSLRLTYRNLSGPDKR 432
             ::| |||:| : || ||:|||:| |::: : || | ||:|||:|
Db 389 IAASARTAAEGEGTLESEPAVQVTEVTATSGLVSWGLGRPADPVWMFQIQYN--SSEDET 446

Qy 433 LVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEA------CGEAHTPPAVHSN 487
            |: |:|||::| | | |: ||:|| |::||| |||||| ||||| || |
Db 447 LIYRIVPASSHHFLLKGHLVPGADYDLCLLALSPAAGPSDLTATRLLGCAHFSTLPANPLC 506

Qy 488 HAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGPGAGPL 547
            || | ||| :|| ::| ||:|:||| ||||| |||| | ||:|
Db 507 HALQAHVLGGTLTV---AVGGVLVAALLVFTVALLV-RGRG-----------AGNGRLPL 551

Qy 548 ELEGVKVPLEPGPKATEGGGEALP 571
             :| :| || ||
Db 552 KLSHVQ------SQTNGGTSPMP 568

RESULT 11
Q3UVS6_MOUSE
ID   Q3UVS6_MOUSE   PRELIMINARY;   PRT;   634 AA.
AC   Q3UVS6;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.

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DT   18-APR-2006, entry version 8.
DE   12 days embryo embryonic body between diaphragm region and neck cDNA,
DE   RIKEN full-length enriched library, clone:9430023110
DE   product:Fibronectin leucine rich transmembrane protein 2, full insert
DE   sequence.
GN   Name=Map4k5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC   neck;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 30:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC   neck;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC   neck;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]

RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC   neck;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang H., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC   neck;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC   neck;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC   neck;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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Qy  221 ARNPFNCVCPLSWFGPWVRRSHVTLASPEETRCHPPKNAGRLLLELDYADFGCPATTTT  280
            ||   |         |||         ||    |  |   |  ||  :||   |
Db  308 RNNPWFCDCSIKWVTEWLKYIPSSL-NVRGFMCQGPEQVRGMAVRELNMNLLSCPTTTPG 366

Qy  281 ATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPDCPPSTCL   340
            |  |  |             |              |         ::
Db  367 LPVFTPAP--------STVSPTTQSPTL-----SVPSPSRGSVPPAPTPSKLPTIPDW    411

Qy  341 NGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTS  400
            :|                                    |||
Db  412 DG-----------------RERVTPPISERIQLSIHFVNDTS                   436

Qy  401 LRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY-TVTQLRPNATYSVC  459
            | |     ||   | ||:| |    | |    | ||  :| |    |::|   ::| |
Db  437 IQVSWLSLFTVMAYKLTWVKMGHSLVGG----IVQERIVSGEKQHLSLVNLEPRSTYRIC  492

Qy  460 VMPLGPGPRVPEGEEA-CGEAHTPPA------VHSNHAPVTQAREGNLPLLIAPALAAVL  511
            : || || | ||:    |  ||           ||    |   : ||||| || | |
Db  493 LVPLDAFNYRTVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGS-PFLLAGLIGGAV  551

Qy  512 LAALAAVGAAYC---VRRGR                                         528
            : | |  |     ::||
Db  552 IFVLVVLLSVFCWHMHKKGR                                         571


RESULT 12
Q8BLU0_MOUSE
ID   Q8BLU0_MOUSE            PRELIMINARY;      PRT;    660 AA.
AC   Q8BLU0;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   27-JUN-2006, entry version 30.
DE   Adult male aorta and vein cDNA, RIKEN full-length enriched library,
DE   clone:A530098L04 product:LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN
DE   FLRT2 homolog (10 days neonate cerebellum cDNA, RIKEN full-length
DE   enriched library, clone:653042IA03 product:Fibronectin leucine rich
DE   transmembrane protein 2, full insert sequence) (Fibronectin leucine
DE   rich transmembrane protein 2).
GN   Name=Flrt2; Synonyms=Map4k5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;
RX   MEDLINE=9927253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 30:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa H.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
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RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Suni Y., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Embryonic body between diaphragm region and
RC   neck;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano N., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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CC
DR   EMBL; AK136973; BAE23193.1; -; mRNA.
DR   MGI; MGI:1925503; Map4k5.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000448; LRR_C.
DR   InterPro; IPR000372; LRR_cys_N.
DR   InterPro; IPR003591; LRR_N.
DR   InterPro; IPR013090; LRR_typ.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00560; LRR_1; 9.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00369; LRR_TYP; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   PROSITE; PS50053; FN3; 1.
DR   PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
KW   Leucine-rich repeat; Membrane; Repeat; Transmembrane.
SQ   SEQUENCE   634 AA;  71069 MW;  097196FE607D8085 CRC64;

Query Match             10.9%;  Score 341;  DB 2;  Length 634;
Best Local Similarity   23.1%;
Matches  143;           Conservative   85;  Mismatches  238;  Indels  154;  Gaps   19;

Qy    4 RVPLLLPLILLLALGPGVQ----GCPSGGQCSQPDTVFCTARQTTVPRDVPPDTVGLY    58
          |:|:|||: |:||:|||         ::|          |     ::
Db   11 RGAFILKFWLIISLGLYLQVSKLLACPSVCRCDR-NFVYCNERSLTSVPLGIPEGVTVLY  69

Qy   59 VF----------------------------------------------ENGITMLDASSF  72
         :
Db   70 LHNNQINNAGFPAELHNVQSVHTVTVLYGNQLDEFPMNLPKNVRVLHLQENNIQTISRAAL 129

Qy   73 AGLPGLQLLDLSQNQIASLRLP--------RLLLIDLSHNSLLALEPGI---LDTANVEA  121
          | | | |:|  | ||:| |        |||:||| |||| |:|            :|
Db  130 AQLLKLEELHLDDNSISTVGVEDGAFREAISLKLLFLSKNHLSSVPVGLPVDLQELRVDE  189

Qy  122 LRLA----GLGLQQLD------------EGLFSRLRNLHDLDVSDNQLERVPPVI       160
          | |     | |  |            : ||:  |  |:|| | ||:| | | ::
Db  190 NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPDL  249

Qy  161 RGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAA  220
          |||| |:||:   |  : ::| ||  ||  |:|||:|| | |:|  | |:| ||:|  ::
Db  250 PGTH-LIRLYLQDN-QINHIPLTAFANLRKLERLDISNNQLRMLTQGVFPDHLSNLKQLTA 307
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RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reid J.F., Ring B., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi M., Semple C.A., Seno M., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Cerebellum;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Ishii M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima M., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito S., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda T., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. Metallothionien-TGF alpha model.
RC   10 month old virgin mouse. Taken by biopsy.;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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Query Match      10.9%;    Score 341; DB 2;    Length 660;
Best Local Similarity    23.1%;    Pred. No. 4.4e-11;
Matches  143;    Conservative  85;    Mismatches 238;    Indels 154;    Gaps    19;

Qy     4 RVPLLLPLLLLALGPGVQ----GCPSGGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLY 58
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Db    11 RGAPILKFWLIISLGLYLQVSKLLACPSVCRCDR-NFVVCNERSLTSVPLGIPEGVTVLY 69

Qy    59 VF----------------------------------ENGITMLDASSF 72
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Db    70 LHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTISRAAL 129

Qy    73 AGLPGLQLLDLSQNQIASLRLP---------RLLLLDLSHNSLIALEPGI---LDTANVEA 121
           ||:   :::   ::                  ::
Db   130 AQLLKLEELHLDDNSISTVGVEDGAFREAISLKLLFLSKNHLSSVPVGLPVDLQELRVDE 189

Qy   122 LRLA--GLGLQOLD-------------------EGLFSRLRLNLHDLDVSDNQLERVPPVI 160
           |||   ||:||:|                     ||| :| |: | ||:|||::
Db   190 NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPDL 249

Qy   161 RGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAA 220
           |  |::|  | :|  :  : :|| | |    |:   :|:: |  | |  |:|  |:
Db   250 PGTH-LIRLYLQDN-QINHIPLTAFANLRKLERLDISNNQLRMLTQGVFDHLSNLKQLTA 307

Qy   221 ARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLELDYADFGCPATTTT 280
           ||        |:       |   | :  :  | :|| |  | ::|    | |
Db   308 RNNPWFCDCSIKWVTEWLKYIPSSL-NVRGFMCQGPEQVRGMAVRELNMNLLSCPTTTPG 366

Qy   281 ATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVGPVQPQPQDCPPSTCL 340
           |:  :     | |   |  ::  :  |  :  |
Db   367 LPVFTPAP--------STVSPTTQSPTL------SVPBPSRGSVPPAPTPSKLPTIPDW 411

Qy   341 NGGTCHLGTRHHLACLCPEGFTGLYCESOMGQGTRPSPTPTPRPPRSLTLGIEPVSPTS 400
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Db   412 DG---------------------------RERVTPPISERIQLSIHFVNDTS 436

Qy   401 LRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY-TVIQLRPNATYSVC 459
           ::|   |   :  ||: :  :| :|  || |:| :::::| :  :|
Db   437 IQVSWLSLFTVMAYKLTWVKMGHSLVGG----IVQERIVSGEKQHLSLVNLEPRSTYRIC 492

Qy   460 VMPLGPGRVPEGEEA-CGEAHTPPA------VHSNHAPVTQAREGNLPLLIAPALAAVL 511
           |  | | | |:|:|  |||  | |        |:|| |   |  | |:::| || |
Db   493 LVPLDAFPNYRTVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGS-PFLLAGLIGGAV 551

Qy   512 LAALAAVGAAYC---VRRGR 528
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Db   552 IFVLVLLSVFCWHMHKKGR 571
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RESULT 13
LRC24_MOUSE
ID   LRC24_MOUSE    STANDARD;    PRT;    521 AA.
AC   Q8BHA1;
DT   04-APR-2006, integrated into UniProtKB/Swiss-Prot.
DT   01-MAR-2003, sequence version 1.
DT   30-MAY-2006, entry version 33.
DE   Leucine-rich repeat-containing protein 24 precursor.
GN   Name=Lrrc24;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
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RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory bulb;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass membrane protein
CC       (Potential).
CC   -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC       domain.
CC   -!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.
CC   --------------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   --------------------------------------------------------------------------
DR   EMBL; AK048678; BAC33419.1; -; mRNA.
DR   EMBL; AK078176; BAC37163.1; -; mRNA.
DR   UniGene; Mm.289666; -.
DR   HSSP; Q9B2R6; 1OZN.
DR   Ensembl; ENSMUSG00000033707; Mus musculus.
DR   MGI; MGI:3605040; Lrrc24.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR013098; Ig_I-set.
DR   InterPro; IPR003599; Ig_sub.
DR   InterPro; IPR003598; Ig_sub2.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_C.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF07679; I-set; 1.
DR   Pfam; PF05560; LRR_1; 4.
DR   Pfam; PF01463; LRRCT; 1.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00369; LRR_TYP; 3.
DR   SMART; SM00082; LRRCT; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
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KW   Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Membrane;
KW   Repeat; Signal; Transmembrane;
FT   SIGNAL        1     23       Potential.
FT   CHAIN        24    521       Leucine-rich repeat-containing protein
FT                               24.
FT                               /FTId=PRO_000231597.
FT   TRANSMEM    414    434       Potential.
FT   REPEAT       57     80       LRR 1.
FT   REPEAT       81    104       LRR 2.
FT   REPEAT      106    128       LRR 3.
FT   REPEAT      130    152       LRR 4.
FT   REPEAT      153    176       LRR 5.
FT   REPEAT      178    200       LRR 6.
FT   REPEAT      252    273       LRR 7.
FT   DOMAIN      268    371       Ig-like C2-type.
FT   COMBIAS     435    440       Poly-Arg.
FT   CARBOHYD     91     91       N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD    342    342       N-linked (GlcNAc...)  (Potential).
FT   CARBOHYD    371    371       N-linked (GlcNAc...)  (Potential).
FT   DISULFID    289    353       By similarity.
SQ   SEQUENCE   521 AA;  56334 MW;  3D1E4BEB302284A6 CRC64;

Query Match             10.8%;     Score 339;  DB 1;  Length 521;
Best Local Similarity   27.0%;     Pred. No. 4.5e-11;  Gaps 120;
Matches 149;  Conservative 66;  Mismatches 217;  Indels 120;  Gaps 21;

Qy        1 MCSRVPLLLPL---LLLLALGPGV----QGCPSGCQCSQPQTVFCTARQGTTVPRDVPPD   53
                          : :|||  ||||  ||   :|  | |:|| |:  |   |||::||
Db        1 MALRAPTLLLLLLLGLLLLPLLPGLPPRATGCPAACRC-YSATVECGALRLRVVPPGIPPG   59

Qy       54 TVGLYVFENGITMLDASSFAGLPGLQLDLSQNQIASLR------LPRLLLLDLSHNSLL   107
              |:::|||  ||   |||| :|||| ||  |:| |:|      |||||||||:|| ||
Db       60 TQTLFLQDNSIAHLEQGSLAPLAALRHLYLHNNTLRALESGAFRAQPRLLELALTGNRLR   119

Qy      108 ALEPG--ILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGL   166
               |||    |:  |: |  |||| | |:   | :|:  |  |  ||::::|  || | | |
Db      120 GLRGGAFVGLVQLRVLYLAGNQLAKLLDFTFLHLPRLQELHLQENSIE-------------   167

Qy      167 TRLRLAGNTRIAQLRPEDLAGLAAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFN   226
            ||| ||||  ||||     :|| | |||| :  ||||  || :  |||  :| ||  || :
Db      168 ------------LLEDQALAGLSSLALLDLSRNQLGTISKEALQPLSSLQVLRLTENPWR   215

Qy      227 CVCPLSWFGPWVRESHVTLASPEETR--CHPPPKNAGRLLLELDYADFGCPATTTTATVP   284
            |:|| ::||| |:|: :| ||| |:|   ||    :|  ||| |  : |||    ||::|
Db      216 CDCALHWLGSWIKEGGRRLLSSRDKKITCAEPPRLALQSLLEVSGGSLIC--------IP   267

Qy      285 TTRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPP--STCLNG   342
             |||| |  |:| :: |||| |||| || || ||||  |||||||| ||| |  |||  |
Db      268 PSVNV--EPPBFTANIGED-LQVACQASGYPQP----LVVWRKVFQPRDGKPQAQAQLEG   320

Qy      343 GTCHLG----------------TRHHLACLCPEGFTGLY-CESQMGQGTRPSPTPVTPRPPR   387
            ||| |                  ||:| ||| :|| || |||| |||||| | |||  |||
Db      321 GAPGLGHGHGTRDTGSGMLFLTNITLA------HAGKYECEAANAGGKARVPFHLLVNASR   374

Qy      388 SLTLGI-BPVSPTSLRVGLQGRYLQGSSVQLRSLRLTYRNLSGPDKRLVTL---------   436
             |||| |||:|| |  ||| |:|:|| || || || |:|  ||| ||:|:|
Db      375 QQSQQLPDPQAPATRPVGHEPQHEAGSMAFRALGLATQTAITAAIALLAUTALLLLAAMIC   434

Qy      437 ------RLPASLAEYT-----------------VTQLRPNATYSVCVM----PLGPGRVPE   470
                  :|| |: |                     ||||  || :|||     ||| ||| |
Db      435 RRRRRRKKVPAPSGEGTLFVNDYSDGPCTFAQLEEELRDDHGHEMFVIDRSKPLFPEVLP-   493

Qy      471 GEEACGEAHTPP   482
            ||||   |  ||
Db      494 -EEA--PEHNPP   502

RESULT 14
Q4SGV9_TETNG
ID   Q4SGV9_TETNG            PRELIMINARY;   PRT;   655 AA.
AC   Q4SGV9;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
```

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DT   27-JUN-2006, entry version 8.
DE   Chromosome 14 SCAF14590, whole genome shotgun sequence. (Fragment).
GN   ORFNames=GSTENG00018451001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli L., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; CAAE01014590; CAG00123.1; -; Genomic_DNA.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_C.
DR   InterPro; IPR000372; LRR_cys_N.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00560; LRR_1; 8.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00369; LRR_TYP; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   PROSITE; PS50853; FN3; 1.
FT   NON_TER       1      1
FT   NON_TER     655    655
SQ   SEQUENCE   655 AA;  72743 MW;  8EF3556E5FB1B126 CRC64;

Query Match              10.8%;     Score 338;  DB 2;  Length 655;
Best Local Similarity    25.3%;     Pred. No. 6.5e-11;
Matches 160;  Conservative 78;  Mismatches 206;  Indels 188;  Gaps 31;

Qy        7 LLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPR-----------------   48
            |:|  || ::|  ||| ||:| :|| |||:|:|  |||||
Db       13 LTVTLSLQVRLGRGA-SCPQECRCDN-TFVYCNERSLTSVPLGIQEGYKVFLHNNQINN   70

Qy       49 ------------------------------DVPPDTVGLYVFENGITMLDASSFAGLPGLQL   80
                                          ||  |||||||||  ||::||  |  ||||| |
Db       71 AGFPVELHHLASVETVHLYGNQLDEFFINLPKNTRVLHLQENNIQTISRAALAQLTRLEE   130

Qy       81 LDLSQNQIASLRLPR----------LLLLDLSHNSLLALEPGI---LDTANVEALRLAGLG-   128
            |||:| | :|||:|           |||||:|:|: ||||||     ||||| :| |||
Db      131 LHLDDNSISTVGVEEGAFREAVSLKLLFLTKNHLSSVPIGLPEELEELRLDENRIAVIAE   190
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DR   InterPro; IPR003591; LRR_typ.
DR   InterPro; IPR013090; Phospholip_A2_AS.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00560; LRR_1; 9.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00369; LRR_TYP; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   PROSITE; PS50853; FN3; 1.
DR   PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
FT   NON_TER      1
SQ   SEQUENCE   637 AA;   71302 MW;  9577AD980D67162F CRC64;

Query Match            10.6%;   Score 332;  DB 2;  Length 637;
Best Local Similarity  23.2%;   Pred. No. 1.4e-10;
Matches   142;  Conservative   81;  Mismatches  233;  Indels  156;  Gaps   19;

Qy    7  LLLPLLLLALGPGVGQVCGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLVVF------   60
            :::  |||  : ::::
Db    3  LYLQVSKLLA-------CPSVCRCDR-NFVYCNERSLTSVPLGIPEGVTVLYLHNNQINN   54

Qy   61  ------------------------------------------ENGITMLDASSPAGLPGLQL   80
                                                      ||:  :  ::
Db   55  AGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTISRAALAQLLKLEE   114

Qy   81  LDLSQNQIASLRLP---------RLLLLDLSHNSLLALEPGI----LDTANVEALRLA------G   126
           ||| ::::       ::::                    :::
Db  115  LHLDDNSISTVGVEDGAFREAISLKLLFLSKNHLSSVPVGLPVDLQELRVDENRIAVISD   174

Qy  127  LGLQQLD-----------------EGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTR-LIR   168
           :                       ||
Db  175  MAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPDLPGTH-LIR   233

Qy  169  LRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCV   228
           ||: | ||   |:::    ||     :::  ||
Db  234  LYLQDN-QINHIPLTAFANLRKLERLDISNNQLRMLTQGVFDHLSNLKQLTARNNPWFCD   292

Qy  229  CPLSWFGPWVRESHVTLASPEETRCHFPPPKNAGRLLLELDYADFGCPATTTTATVPTTRP   288
           | | ||||| ::::         |  :::      ||
Db  293  CSIKWVTEWLKYIPSSL-NVRGFMCCQQPEQVRGMAVRELNMNLLSCPTTTPGLPVFTPAP   351

Qy  289  VVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLG   348
           ||    ::::  ||||   |
Db  352  --------STVSPTTQSPTL------SVPSPSRGSVPPAFTPSKLPTIPDWDG-------   390

Qy  349  TRHHLACLCPEGFTGLYCESQMGQGQTRPSPTTVTPRPPRSLTLGIEPVSPTSLRVGLQRY   408
           |||
Db  391  ------------------------------------------RERVTPPISERIQLSIHFVNDTSIQVSWLSL   421

Qy  409  LQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY-TVTQLRPNATYSVCVMPLGPGR   467
           :::  ::::       |::         ||  :: :::    ||
Db  422  FTVMAYKLTWVKMGHSLVGG---IVQERIVSGEKQHLSLVNLEPRSTYRICLVPLDAFN   477

Qy  468  VPEGEA-CGEAHTPPA------------VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVG   519
           ||              ||           |:::   |        |||||::::::::
Db  478  YRTVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGS-PFLLAGLIGGAVIFVLVLL   536

Qy  520  AAYC--VRRGR   528
           ::||   :|::
Db  537  SVFCWHMHKKGR   548


Qy  129  ------LQQL-------DEGL---FSRLRNLHDLDVSDNQLERVPPVIRGLRGLTR   168
                 :::|          ||||      ||
Db  191  EAFQNVTRLQRLLLDGNLLTDEGIAPGTFQDLVNLRELALARNSLTFPPLLPG-RALFR   249

Qy  169  LRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQAL-PGDLSGLFPRLRLLAAARNPFNC   227
           |:| :::|    |: ::    ||     :::   | |         ||
Db  250  LSLQEN-QIDQIPVAAFAGLHRLEKLDVSSNQLQSLTQGVFEGL-GALRHLMVRNNPWRC   307

Qy  228  VCPLSWFGPWVRESHVTLASPEETR---CHFPPPKNAGRLLLELDYADFGCPATTTTATVP   284
           | | |||||       ::::       |
Db  308  DCAVKWVVVWLR----SLPASVNARGFVCQSPEKVRGMAIRELTLDVIECP--------   354

Qy  285  TTRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGT   344
           ||              |||| |       |
Db  355  ------PGAGS----PSW--PTLRST-PPPPPTTAPTTTATAGSTAITPP-------   391

Qy  345  CHLGTRHHLACLCPEGFTGLYCESQMGQGQTRPSPT----PVTPRPPRS--LTLGIEPVSP   398
           |                 :::    |||||||
Db  392  IPYYFES------SSPPVPSLRNNPPGPLPPYEDPLQIYHVVNS   430

Qy  399  TSLRVGLQRYLQGSSVQLRSLRLTY-----RNLSGPDKRLVTLRLPASLAEYTVTQLRP   452
           ::::       |::         |        |::
Db  431  SNIEVSWASYF------TVTAYKVTWKRGQGQTNEGPRERTV----GGDQRRISLGNLEP   481

Qy  453  NATYSVCVMPLG------PGRVPEGEEACGEAHTPPAVHS-----NHAPVTQAREG-NLP   500
           | :::  |          ||   ||          |        |::
Db  482  RSVRRICVHVLDTLNSYRPGE----DTLCSEARTKAAASTKAPGRDHAP----QEGIHST   533

Qy  501  LLIAPALAAVLLAALAAVGAAYC--VRRGRA   529
           |||||::::::::      ::||   :||:|
Db  534  LLMAGIIGGAVLLVLATLLGLFCWHVHRKSRA   565


RESULT 15
Q6A073_MOUSE
ID   Q6A073_MOUSE     PRELIMINARY;     PRT;    637 AA.
AC   Q6A073;
DT   13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2004, sequence version 1.
DT   27-JUN-2006, entry version 19.
DE   MKIAA0405 protein (Fragment).
GN   Name=Map4k5; Synonyms=Flrt2, mKIAA0405;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   PubMed=15368895; DOI=10.1093/dnares/11.3.205;
RA   Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA   Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA   Nagase T., Ohara O., Koga H.;
RT   "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT   IV. The complete nucleotide sequences of 500 mouse KIAA-homologous
RT   cDNAs identified by screening of terminal sequences of cDNA clones
RT   randomly sampled from size-fractionated libraries.";
RL   DNA Res. 11:205-218(2004).
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DR   EMBL; AK172945; BAD32223.1; -; mRNA.
DR   Ensembl; ENSMUSG00000047414; Mus musculus.
DR   MGI; MGI:3603594; Flrt2.
DR   MGI; MGI:1925503; Map4k5.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_C.
DR   InterPro; IPR000372; LRR_cys_N.
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Search completed: January 28, 2007, 17:34:01
Job time : 379 secs

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                    GenCore version 6.2
         Copyright (c) 1993 - 2007 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:   January 28, 2007, 17:26:16 ; Search time 44 Seconds
                              (without alignments)
                              1307.673 Million cell updates/sec

Title:       US-10-677-669-69
Perfect score: 3135
Sequence:    1 MCSRVPLLPLLPLLLLALGPG..........PLMGFPGPGLQSPLHAKPYI 598

Scoring table: BLOSUM62
          Gapop 10.0 , Gapext 0.5

Searched:    283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:    283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :    PIR 80:*
         1:   pir1:*
         2:   pir2:*
         3:   pir3:*
         4:   pir4:*

           *
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                         SUMMARIES
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Result No.	Score	Query Match	Length	DB	ID	Description
1	322	10.3	605	2	JC5239	insulin-like growt
2	302	9.6	605	1	A41915	insulin-like growt
3	282	9.0	626	1	NBHUIA	platelet glycoprot
4	281.5	9.0	603	2	JC1282	insulin-like growt
5	278.5	8.9	603	2	JC6128	insulin-like growt
6	278	8.9	1531	2	T42218	slit-1 protein hom
7	264.5	8.4	420	2	A53531	oncofetal trophobl
8	261	8.3	1523	2	T13953	MEGF5 protein - ra
9	255.5	8.1	1469	2	B36665	slit protein 2 pre
10	255.5	8.1	1480	2	A36665	slit protein 1 pre
11	251	8.0	622	2	JC7973	synleurin - human
12	243.5	7.8	312	1	NBHUA2	leucine-rich alpha
13	240	7.7	560	2	A60164	platelet membrane
14	237	7.6	707	2	JC7763	neuronal leucine-r
15	231	7.4	1025	2	T42626	secreted leucine-r
16	222.5	7.1	536	2	A34901	lysine carboxypept
17	214.5	6.8	1535	2	S46224	peroxidasin - frui
18	212.5	6.8	361	2	A53860	chondroadherin pre
19	210.5	6.7	4302	2	A38971	polycystic kidney
20	209	6.7	1091	2	A58532	glial cell membran
21	208.5	6.7	382	2	I39068	proline- arginine-
22	200	6.4	653	2	T25194	hypothetical prote
23	199	6.3	1328	2	T23007	hypothetical prote
24	194.5	6.2	789	2	T28714	hypothetical prote
25	194.5	6.2	1355	2	T28715	hypothetical prote
26	193.5	6.2	421	2	T46266	hypothetical prote
27	193.5	6.2	721	2	E70766	hypothetical prote
28	192.5	6.1	575	2	T29972	hypothetical prote
29	189	6.0	369	2	S20811	proteoglycan I - m
30	189	6.0	369	2	S32793	biglycan precursor
31	189	6.0	839	2	T04859	extensin homolog F
32	188.5	5.9	440	2	A47530	oligodendrocyte-my
33	184	5.8	440	2	A39613	oligodendrocyte-my
34	183	5.8	368	1	BGHUN	garp precursor - h
35	182	5.8	662	2	S42799	biglycan precursor
36	181.5	5.7	369	2	S32559	decorin precursor
37	177.5	5.6	357	2	S24317	adenylate cyclase
38	176.5	5.6	2493	2	A55481	densin-180 - rat
39	175	5.5	1495	2	T11434	lumican precursor
40	173	5.5	343	2	A41748	G protein-coupled
41	172.5	5.5	925	2	JC2033	decorin precursor
42	172	5.5	359	1	NBHUC8	hypothetical prote
43	170.5	5.4	1134	2	T04587	adenylate cyclase
44	170	5.4	2145	2	JC4747	orphan G protein-c
45	169.5	5.4	907	2	JE0176	extensin homolog T
46	169	5.4	760	2	T06291	decorin precursor
47	169	5.4	354	2	A55454	hypothetical prote
48	168.5	5.4	839	2	F75518	G protein-coupled
49	167	5.3	907	2	JG0193	internalin A precu
50	167	5.3	800	2	S37387	disease resistance
51	166.5	5.3	1112	1	T10504	hypothetical prote
52	166.5	5.3	549	2	T41744	Internalin A (impo
53	165.5	5.3	800	2	AB1129	decorin precursor
54	165.5	5.3	360	2	S06280	hypothetical prote
55	165.5	5.3	526	2	C84552	gene flightless-I
56	165.5	5.3	1256	2	S60461	flightless-I homol
57	165	5.3	1268	2	A49674	probable disease r
58	165	5.2	994	2	H96510	extensin homolog F
59	163.5	5.2	786	2	T01456	hypothetical prote
60	162	5.2	242	2	T14791	Ras-binding protei
61	161	5.1	559	2	T42998	cell-surface molec
62	161	5.1	682	2	A49121	connectin precurso
63	161	5.1	682	2	A43318	ocogelin - mouse
64	160.5	5.1	2910	2	T42214	hypothetical prote
65	160	5.1	744	2	E86255	hypothetical prote
66	159.5	5.1	1112	2	T00952	protein AC7.2 [imp
67	159	5.1	572	2	T30947	hypothetical prote
68	159	5.1	613	2	A88684	leucine-rich-repea
69	159	5.1	702	2	T21148	hypothetical prote
70	159	5.1	1119	2	AD1822	hypothetical prote
71	158.5	5.1	738	2	T19938	hypothetical prote
72	158	5.0	1066	2	T15864	mucin MUC5B, trach
73	158	5.0	3570	2	T45025	decorin - rabbit
74	156.5	5.0	360	2	I47020	probable receptor-
75	156.5	5.0	980	2	H84632	decorin precursor
76	156	5.0	354	2	S29145	hypothetical prote
77	156	5.0	594	2	T23841	N-chimerin homolog
78	155.5	5.0	903	2	T00705	probable multi-dom
79	155.5	4.9	1334	2	T50568	hypothetical prote
80	155	4.9	961	2	T23395	probable serine/th
81	154.5	4.9	1013	2	T10659	receptor-like prot
82	154.5	4.9	1143	2	T10636	transcription co-r
83	154.5	4.9	1192	2	T48499	protein kinase hom
84	154.5	4.9	1495	2	S60255	protein-tyrosine k
85	153.5	4.9	864	2	T08575	US4 protein - huma
86	153.5	4.9	894	1	A41527	Toll protein-like
87	153	4.8	699	2	C43674	follitropin recept
88	152	4.8	786	2	T08664	leucine-rich prote
89	151.5	4.8	695	1	JN0898	gene wheeler prote
90	151	4.8	540	2	T12704	receptor-like prot
91	151	4.8	1389	2	T13852	chaoptin precursor
92	150.5	4.8	695	1	QRHUFT	hypothetical prote
93	150.5	4.8	1109	1	T18536	follitropin recept
94	150	4.8	1134	2	A29944	protein kinase Xa2
95	149.5	4.8	224	2	T32185	probable receptor
96	149.5	4.8	696	1	JC7361	class VII unconven
97	149	4.8	1025	2	A57676	fibromodulin precu
98	149	4.8	1143	2	B84431	hypothetical prote
99	149	4.8	2357	1	A59249	hypothetical prote
100	148.5	4.7	375	2	S05390	hypothetical prote
101	148.5	4.7	610	2	T23836	hypothetical prote
102	148.5	4.7	680	2	T19939	hypothetical prote

#					ID	Description
103	148.5	4.7	890	2	C96654	hypothetical prote
104	148.5	4.7	964	2	T49038	hypothetical prote
105	148.5	4.7	1115	2	S40241	G protein-coupled
106	148	4.7	338	2	S52284	lumican, secretory
107	148	4.7	1188	2	S49915	extensin-like prot
108	147.5	4.7	316	2	A41781	proteoglycan-Lb -
109	147.5	4.7	1385	2	T13887	tlr protein - frui
110	147	4.7	1964	2	T09059	notch4 - mouse
111	147	4.7	2414	2	A54277	transcription adap
112	146.5	4.7	382	2	T04260	hypothetical prote
113	146.5	4.7	925	2	C84538	probable LRR recep
114	146.5	4.7	1408	2	S16108	gene serrate prote
115	146	4.7	369	2	G83434	translocation prot
116	145.5	4.6	380	2	S71876	fibromodulin - chi
117	145.5	4.6	886	2	S29605	glycoprotein 350/2
118	145.5	4.6	2142	2	B35098	MHC class III hist
119	145	4.6	458	2	T19941	hypothetical prote
120	145	4.6	679	2	T20713	hypothetical prote
121	145	4.6	694	2	JC2237	follitropin recept
122	145	4.6	1839	1	OYBYK	adenylate cyclase
123	144.5	4.6	486	2	B86460	hypothetical prote
124	144.5	4.6	2187	1	T30826	nascent polypeptid
125	144.5	4.6	3149	1	QQBE8	BPLF1 protein - hu
126	144	4.6	695	2	I45896	follicle stimulati
127	144	4.6	1019	2	C96519	probable disease r
128	144	4.6	3020	2	A43932	mucin 2 precursor,
129	143.5	4.6	243	2	B41710	promastigote surfa
130	143.5	4.6	476	2	T27051	hypothetical prote
131	143.5	4.6	496	2	C96832	hypothetical prote
132	143.5	4.6	605	2	T50817	protein serine/thr
133	143.5	4.6	683	2	T24486	hypothetical prote
134	142.5	4.5	1870	2	S37671	MHC class III hist
135	142.5	4.5	1872	2	S36152	MHC class III hist
136	142	4.5	661	2	I56258	RP105 - mouse
137	142	4.5	983	2	G84524	probable disease r
138	141.5	4.5	462	2	D84858	hypothetical prote
139	141.5	4.5	836	2	T46070	hypothetical prote
140	141.5	4.5	1029	2	T05050	protein kinase hom
141	141.5	4.5	1051	2	T13174	gp150 protein - fr
142	141	4.5	630	2	AC1129	internalin B [impo
143	141	4.5	717	2	T33295	hypothetical prote
144	140.5	4.5	376	2	S55275	fibromodulin precu
145	140	4.5	277	2	I60122	rsu-1 homolog - hu
146	140	4.5	474	2	S65763	chitinase (EC 3.2.
147	140	4.5	754	2	A85043	probable LRR recep
148	140	4.5	1029	2	T00712	protein kinase hom
149	139.5	4.4	333	2	T34555	hypothetical prote
150	139.5	4.4	527	2	A75399	probable disease r
151	139.5	4.4	539	2	G70520	hypothetical prote
152	139.5	4.4	4351	2	T00252	MEGF1 protein - ra
153	139	4.4	581	2	A45551	insect-stage-speci
154	139	4.4	603	2	T24315	hypothetical prote
155	139	4.4	720	2	T02361	hypothetical prote
156	139	4.4	1088	2	E86321	F11A6.9 protein -
157	139	4.4	2240	2	T37057	probable multi-dom
158	138.5	4.4	342	2	A46743	lumican precursor
159	138.5	4.4	990	2	T14756	hypothetical prote
160	138.5	4.4	1650	2	S53457	dominant autoantig
161	138	4.4	630	2	C39930	hypothetical prote
162	138	4.4	858	2	T00258	hypothetical prote
163	138	4.4	1952	2	T48814	hypothetical prote
164	137.5	4.4	1151	2	T18535	high molecular mas
165	137.5	4.4	4660	1	T42737	gp330 protein prec
166	137	4.4	562	2	T34319	hypothetical prote
167	137	4.4	695	2	JC1493	follitropin recept
168	137	4.4	788	2	AG0786	secreted effector
169	137	4.3	907	1	QQBE21	membrane antigen g
170	137	4.4	4544	1	S02392	alpha-2-macroglobu
171	136.5	4.4	4545	1	S25111	alpha-2-macroglobu
172	136	4.3	322	2	S72271	proteoglycan Lb pr
173	136	4.3	626	2	AE0123	probable antigenic
174	136	4.3	692	2	A34548	follitropin recept
175	136	4.3	1008	2	D84434	probable receptor-

#					ID	Description
176	136	4.3	4957	2	T03455	ALR protein - huma
177	135.5	4.3	427	2	JC4915	ags protein precur
178	135.5	4.3	499	2	D83333	hypothetical prote
179	135.5	4.3	1124	2	B84742	probable receptor-
180	135.5	4.3	5262	2	T03454	ALR protein - huma
181	135	4.3	601	2	S56144	SH3 domain binding
182	134.5	4.3	613	2	T15489	hypothetical prote
183	134.5	4.3	847	2	F96531	hypothetical prote
184	134.5	4.3	1039	2	T22117	hypothetical prote
185	134	4.3	530	2	A45690	transactivator EBN
186	134	4.3	656	2	B47096	hy1B homolog - Str
187	134	4.3	886	2	T40734	probable adenylate
188	133.5	4.3	277	2	S25770	RSP-1 protein - mo
189	133.5	4.3	384	2	A41710	promastigote surfa
190	133.5	4.3	1068	2	H96769	hypothetical prote
191	133	4.2	576	2	T36729	probable serine/th
192	133	4.2	852	2	I51259	tyrosine kinase C
193	133	4.2	932	2	T48489	receptor-like prot
194	133	4.2	1257	2	A88536	protein B0523.5 [i
195	133	4.2	4391	2	A38096	perlecan precursor
196	132.5	4.2	463	1	A36479	milk fat globule m
197	132.5	4.2	2035	2	A40718	host cell factor C
198	132	4.2	3164	1	WMBEH6	UL36 protein - hum
199	131.5	4.2	346	2	T46916	hypothetical prote
200	131.5	4.2	890	2	T00800	disease resistance
201	131.5	4.2	1097	2	A29943	Toll protein precu
202	131.5	4.2	1286	2	A88396	protein M01E10.2 [
203	131	4.2	612	2	T10727	protein kinase Xa2
204	131	4.2	767	2	B84594	probable LRR recep
205	131	4.2	905	2	T00475	probable disease r
206	131	4.2	915	2	T09575	smoothelin - human
207	131	4.2	1095	2	G96746	hypothetical prote
208	131	4.2	1196	2	T09356	brassinosteroid-in
209	130.5	4.2	448	2	T27395	hypothetical prote
210	130	4.1	268	2	T19697	hypothetical prote
211	130	4.1	389	2	H86266	hypothetical prote
212	130	4.1	395	2	H75457	hypothetical prote
213	130	4.1	768	2	T17462	disease resistance
214	130	4.1	800	2	H84740	hypothetical prote
215	129.5	4.1	315	2	T06806	proline rich prote
216	129.5	4.1	780	2	T00366	hypothetical prote
217	129.5	4.1	861	2	A48825	Notch homolog Motc
218	129.5	4.1	912	2	A54423	brevican precursor
219	129.5	4.1	942	2	S23251	protein-tyrosine k
220	129.5	4.1	1173	2	I50620	procKr2 - chicken
221	129.5	4.1	1469	2	T09219	basal transcriptio
222	129	4.1	371	2	S20075	promastigote surfa
223	129	4.1	835	2	T05259	probable disease r
224	129	4.1	910	2	B96770	hypothetical prote
225	129	4.1	1027	2	B85089	receptor protein k
226	129	4.1	1064	2	B86465	probable Protein k
227	129	4.1	1232	2	T05322	hypothetical prote
228	129	4.1	1329	2	A64828	cell division prot
229	129	4.1	1342	2	E85614	cell division prot
230	129	4.1	1342	2	G90750	cell division prot
231	129	4.1	1959	1	AGRT	agrin - rat
232	129	4.1	2321	2	S78549	notch3 protein - h
233	128.5	4.1	487	2	S42442	nuclear protein EB
234	128.5	4.1	677	2	H86208	protein F22G5.26 [
235	128.5	4.1	727	2	C84534	hypothetical prote
236	128.5	4.1	744	2	C84527	probable receptor-
237	128.5	4.1	825	2	T29634	hypothetical prote
238	128.5	4.1	1113	2	T00271	hypothetical prote
239	128.5	4.1	3968	2	A44265	trithorax homolog
240	128	4.1	597	2	S72468	probable transcrip
241	128	4.1	967	2	T48210	hypothetical prote
242	128	4.1	1428	2	T08852	lustrin A - Califo
243	128	4.1	1914	2	T42635	tenascin Y precurs
244	127.5	4.1	750	2	D86245	hypothetical prote
245	127.5	4.1	1120	2	B86479	hypothetical prote
246	127.5	4.1	1784	2	C96615	hypothetical prote
247	127	4.1	327	2	S20074	promastigote surfa
248	127	4.1	773	2	T00502	probable receptor-

No.	Value	Score	Length	Accession	Count	Description
249	127	4.1	775	EDBE11	1	immediate-early pr
250	127	4.1	800	G84740	1	hypothetical prote
251	127	4.1	1366	T35985	1	probable large Pro
252	127	4.1	1895	T06609	1	disease resistance
253	127	4.1	1955	AGCH	1	agrin precursor -
254	126.5	4.0	268	T45616	2	hypothetical prote
255	126.5	4.0	685	JC7570	2	latent transformin
256	126.5	4.0	694	JC4301	2	follitropin recept
257	126.5	4.0	862	T46289	2	Delta-4 protein -
258	126.5	4.0	999	S27756	1	receptor-like prot
259	126.5	4.0	1091	S33596	2	protein-tyrosine k
260	126.5	4.0	1777	T34369	2	hypothetical prote
261	126	4.0	500	S49302	2	AWJL218 protein -
262	126	4.0	865	A47282	2	calcium-binding pr
263	126	4.0	873	A47283	2	calphotin - fruit
264	126	4.0	996	F86410	2	protein F3M18.12 [
265	126	4.0	1152	T31911	2	hypothetical prote
266	126	4.0	1820	A55494	2	latent transformin
267	125.5	4.0	283	S13383	2	hydroxyproline-ric
268	125.5	4.0	548	AH1107	2	internalin H [impo
269	125.5	4.0	635	F75477	2	hypothetical prote
270	125.5	4.0	764	A40077	2	thyrotropin recept
271	125.5	4.0	1003	T05898	2	hypothetical prote
272	125	4.0	350	S22456	2	hydroxyproline-ric
273	125	4.0	476	A36478	2	surface glycoprote
274	125	4.0	783	T45899	2	receptor protein k
275	125	4.0	818	F96586	2	hypothetical prote
276	125	4.0	991	T52400	2	receptor-like prot
277	125	4.0	1504	T49896	2	glycine/proline-ri
278	125	4.0	2026	OYBY	1	adenylate cyclase
279	124.5	4.0	298	B35272	2	osteoinductive fac
280	124.5	4.0	756	T27642	2	hypothetical prote
281	124.5	4.0	849	C97303	2	hypothetical prote
282	124.5	4.0	910	G84648	2	probable disease r
283	124.5	4.0	977	C96745	2	hypothetical prote
284	124.5	4.0	1223	E88451	2	protein K10D2.1 [i
285	124.5	4.0	2176	T13806	2	toucan gene protei
286	124	4.0	496	D75261	2	conserved hypothet
287	124	4.0	543	S35047	2	mucin JUL7 - human
288	124	4.0	574	T43556	2	Wiskott-Aldrich sy
289	124	4.0	605	AG0123	2	probable antigenic
290	124	4.0	729	E70803	2	hypothetical prote
291	124	4.0	766	B85440	2	receptor kinase-li
292	124	4.0	978	E96787	2	protein T4O12.5 [i
293	124	4.0	1011	T45718	2	receptor-kinase li
294	124	4.0	1472	B54774	2	ATP binding casset
295	124	3.9	4135	T42629	2	tenascin-X - bovin
296	123.5	3.9	380	T01281	2	probable leucine-r
297	123.5	3.9	492	F86263	2	hypothetical prote
298	123.5	3.9	656	AE1479	2	probable cell surf
299	123.5	3.9	690	T41296	2	probable alcohol d
300	123	3.9	528	T15198	2	hypothetical prote
301	123	3.9	574	T38819	2	wiskott-aldrich sy
302	123	3.9	888	S23065	2	ufo protein - mous
303	123	3.9	1072	A37127	2	microtubule-associ
304	122.5	3.9	2591	T30288	2	pristinamycin I sy
305	122.5	3.9	303	S28264	2	hydroxyproline-ric
306	122.5	3.9	415	T13435	2	hypothetical prote
307	122.5	3.9	592	D70863	2	extensin homolog F
308	122.5	3.9	699	T05225	2	probable receptor-
309	122.5	3.9	809	B84634	2	hypothetical prote
310	122.5	3.9	845	T12537	2	disease resistance
311	122.5	3.9	1016	T30553	2	collagen alpha 1(V
312	122.5	3.9	2944	A54849	2	osteoglycin precur
313	122	3.9	298	JC4130	2	hypothetical prote
314	122	3.9	326	T24722	2	internalin like pr
315	122	3.9	596	AE1515	2	probable receptor-
316	122	3.9	623	T19876	2	mucin, tracheal (A
317	122	3.9	672	B84782	2	probable receptor-
318	122	3.9	715	G86239	2	protein F20B24.6 [
319	122	3.9	719	T47727	2	hypothetical prote
320	122	3.9	921	B86234	2	hypothetical prote
321	122	3.9	992	T05335	2	hypothetical prote

No.	Value	Score	Length	Accession	Count	Description
322	121.5	3.9	432	E96712	2	unknown protein, 6
323	121.5	3.9	519	T07026	2	ethylene receptor
324	121.5	3.9	635	T07794	2	ethylene receptor
325	121.5	3.9	686	JC7569	2	Delta-4 protein -
326	121.5	3.9	760	F86387	2	probable Pto kinas
327	121.5	3.9	902	T00588	2	hypothetical prote
328	121.5	3.9	1251	A57293	2	latent transformin
329	121.5	3.9	1409	T37188	2	presynaptic activi
330	121.5	3.9	2265	FNBO	1	fibronectin - bovi
331	121.5	3.9	2297	T34918	2	polyketide synthas
332	121.5	3.9	2318	S45306	2	notch 3 protein -
333	121.5	3.9	3530	A59266	2	unconventional myo
334	121	3.9	306	T52340	2	cell wall-plasma m
335	121	3.9	480	T00971	2	probable disease r
336	121	3.9	485	A33647	2	sulfated surface g
337	121	3.9	733	A45301	2	microtubule-associ
338	121	3.9	1203	A49175	2	Motch B protein -
339	121	3.9	1520	T00273	2	hypothetical prote
340	121	3.9	2531	S18188	2	notch protein homo
341	120.5	3.8	753	A35272	2	osteoinductive fac
342	120.5	3.8	821	JQ0532	2	OP protein - Kenne
343	120.5	3.8	855	AB1126	2	internalin, peptid
344	120.5	3.8	976	T17460	2	disease resistance
345	120.5	3.8	976	B84659	2	probable resistanc
346	120.5	3.8	981	T05897	2	protein kinase hom
347	120.5	3.8	987	T50851	2	receptor protein k
348	120.5	3.8	1118	T50850	2	receptor protein k
349	120.5	3.8	1152	A48292	2	mucin, tracheobron
350	120.5	3.8	1722	A33183	2	microtubule-associ
351	120.5	3.8	1778	E88753	2	protein F1C7.4 [i
352	120.5	3.8	3566	AF1116	1	internalin protein
353	120	3.8	361	A40701	1	tenascin-X precurs
354	120	3.8	376	AH1469	2	internalin protein
355	120	3.8	458	S71558	2	probable cell wall
356	120	3.8	892	T31631	1	large structural p
357	120	3.8	962	T09071	2	hypothetical prote
358	120	3.8	1126	T04124	2	SH3 domains-contai
359	120	3.8	1224	T20801	2	receptor-like prot
360	119.5	3.8	267	T40765	2	hypothetical prote
361	119.5	3.8	479	S08314	2	webl protein homol
362	119.5	3.8	660	A31753	2	cell wall glycopro
363	119.5	3.8	1048	T45569	1	transcription fact
364	119.5	3.8	1079	XPBEA9	2	receptor protein k
365	119.5	3.8	1166	C96772	1	large structural p
366	119.5	3.8	1400	F95598	2	probable receptor
367	119.5	3.8	1596	B70963	2	protein F20N2.4 [i
368	119.5	3.8	1643	A35927	2	hypothetical prote
369	119.5	3.8	164	T14274	2	190K DNA-binding p
370	119.5	3.8	352	I53641	2	versican precursor
371	119	3.8	424	S49299	2	mucin 5AC - human
372	119	3.8	550	S27783	2	AWJL172 protein -
373	119	3.8	651	C75557	1	hypothetical prote
374	119	3.8	660	T42644	2	hypothetical prote
375	119	3.8	808	QQBE3	2	hypothetical prote
376	119	3.8	864	T23129	1	BHLF1 protein - hu
377	119	3.8	1006	D84740	2	hypothetical prote
378	119	3.8	1045	T42731	2	probable disease r
379	119	3.8	222	T41119	2	atrophin-1 related
380	118.5	3.8	400	H96711	1	internalin- relate
381	118.5	3.8	677	A39822	2	hypothetical prote
382	118.5	3.8	751	E70722	2	leukosialin precur
383	118.5	3.8	869	AC2098	2	hypothetical prote
384	118.5	3.8	883	A71400	2	probable disease r
385	118.5	3.8	988	S57653	2	disease resistance
386	118.5	3.8	1173	T45717	2	receptor-kinase li
387	118.5	3.8	1356	T25893	2	hypothetical prote
388	118.5	3.8	1607	A45445	2	janusin precursor,
389	118	3.8	294	T02837	2	long chain fatty a
390	118	3.8	599	A37232	2	mucin, tracheal (A
391	118	3.8	667	T10798	2	pherophorin-S - Vo
392	118	3.8	823	S74254	2	homeotic protein s
393	118	3.8	1134	AD1935	2	general secretion
394	118	3.8		JN0711	1	protein-tyrosine k

No.	Name	Accession	Count	Length	Score	Value
395	cell-fate determin	A49128	2	2471	3.8	118
396	hypothetical prote	D85041	2	473	3.7	117.5
397	collagen alpha 2(x	A55576	2	624	3.7	117.5
398	chitinase (EC 3.2.	JW00067	2	660	3.7	117.5
399	protein kinase Xa2	T10725	2	996	3.7	117.5
400	hypothetical prote	D70568	2	1075	3.7	117.5
401	zinc finger protei	I84499	2	1706	3.7	117.5
402	hypothetical prote	T27904	2	431	3.7	117
403	hepatocyte growth	A46688	1	655	3.7	117
404	probable receptor	H96707	2	670	3.7	117
405	transcription fact	JC4245	2	678	3.7	117
406	probable disease r	C84633	2	743	3.7	117
407	hypothetical prote	T29018	2	801	3.7	117
408	probable receptor-	C84668	2	1007	3.7	117
409	probable penicilli	D75399	2	1009	3.7	117
410	agrin - electric r	T43060	2	1328	3.7	117
411	hypothetical prote	T30273	2	1450	3.7	117
412	MEGF6 protein - ra	T13954	2	1574	3.7	117
413	probable multi-dom	T37056	2	2082	3.7	117
414	hypothetical prote	T34434	2	2232	3.7	117
415	mucin 5AC (clone J	S53363	2	279	3.7	116.5
416	chitinase (EC 3.2.	S51939	2	439	3.7	116.5
417	low density lipopr	I38467	2	621	3.7	116.5
418	hypothetical prote	T27632	2	787	3.7	116.5
419	hypothetical prote	T27633	2	794	3.7	116.5
420	protein ZC518.3 [l	A88860	2	828	3.7	116.5
421	C-terminal domain-	T31425	2	1048	3.7	116.5
422	immediate-early pr	A45344	2	1446	3.7	116.5
423	hypothetical prote	T16199	2	2229	3.7	116.5
424	mucin - rat	S24169	2	292	3.7	116.5
425	repellent protein	S71753	2	652	3.7	116
426	hypothetical prote	AH2348	2	660	3.7	116
427	similar to disease	F86308	2	729	3.7	116
428	disease resistance	T02565	2	771	3.7	116
429	hypothetical prote	B97303	2	808	3.7	116
430	Hcr9-0 protein - t	T07039	2	845	3.7	116
431	hypothetical T2 pr	A24938	2	907	3.7	116
432	period protein hom	T00019	2	1291	3.7	116
433	protein-tyrosine-p	T14355	2	1494	3.7	116
434	GT1 protein - mous	T30250	2	1840	3.7	116
435	notch-1 protein -	A46019	2	2531	3.7	116
436	notch protein homo	A40043	2	2555	3.7	116
437	microtubule-associ	A43359	2	2774	3.7	116
438	apomucin precursor	A53715	2	322	3.7	115.5
439	hypothetical prote	AC3061	2	513	3.7	115.5
440	hypothetical prote	D98225	2	513	3.7	115.5
441	gastric mucin (clo	I47141	2	528	3.7	115.5
442	hypothetical prote	T42659	2	696	3.7	115.5
443	extensin-like prot	T49385	2	805	3.7	115.5
444	nuclear antigen EB	S27921	2	946	3.7	115.5
445	internalin, probab	I38533	2	1093	3.7	115.5
446	AF17 protein - hum	S52781	2	1268	3.7	115.5
447	neurocan - mouse	EDBEIF	1	1460	3.7	115.5
448	immediate-early pr	T16305	2	2214	3.7	115.5
449	367K tegument prot	WZBEB6	1	3421	3.7	115.5
450	hypothetical prote	T08549	2	404	3.7	115
451	hypothetical prote	S74728	2	451	3.7	115
452	extensin-like prot	T10741	2	461	3.7	115
453	transcription fact	S22542	1	479	3.7	115
454	internalin, probab	AH1216	2	539	3.7	115
455	hypothetical prote	T01817	2	766	3.7	115
456	Axin homolog Axil	T08423	2	838	3.7	115
457	protein kinase hom	T05414	2	980	3.7	115
458	hypothetical prote	B86308	2	1133	3.7	115
459	jagged protein pre	A56136	2	1220	3.7	115
460	aggrecan precursor	A39086	1	2415	3.7	115
461	hydroxyproline-ric	JQ0985	2	328	3.7	114.5
462	pP47 protein - pig	T11743	2	409	3.7	114.5
463	internalin like pr	AC1469	2	505	3.7	114.5
464	hypothetical prote	T51880	2	606	3.7	114.5
465	hypothetical prote	T27123	2	627	3.6	114.5
466	protein kinase hom	T05606	2	638	3.6	114.5
467	disease resistance	T01104	2	218	3.6	114
468	leukosialin precur	S00842	2	378	3.6	114
469	transcription fact	A34888	1	413	3.6	114
470	mullerian inhibiti	S20100	2	555	3.6	114
471	hypothetical prote	T29695	2	586	3.6	114
472	proline-rich prote	S62057	2	633	3.6	114
473	hypothetical prote	T00388	2	634	3.6	114
474	hypothetical prote	E75468	2	656	3.6	114
475	P-selectin precurs	A42755	2	768	3.6	114
476	period protein hom	T00018	2	1290	3.6	114
477	hypothetical prote	T26063	2	2225	3.6	114
478	mucin (clone PGM-2	S55316	2	317	3.6	113.5
479	brevican - human (	T46256	2	330	3.6	113.5
480	disease resistance	T01102	2	538	3.6	113.5
481	transforming prote	B43817	2	896	3.6	113.5
482	99.9K hypothetical	A86460	2	907	3.6	113.5
483	nuclear antigen EB	QQBE24	1	938	3.6	113.5
484	hypothetical prote	T33476	2	1286	3.6	113.5
485	protein-tyrosine-p	S50893	2	1907	3.6	113.5
486	hypothetical prote	T20566	2	2911	3.6	113.5
487	hypothetical prote	T49908	2	371	3.6	113
488	mucin 7 precursor,	A48018	2	377	3.6	113
489	hypothetical prote	E84527	2	382	3.6	113
490	hypothetical prote	A90888	2	419	3.6	113
491	hypothetical prote	H85729	2	603	3.6	113
492	probable N-acetylm	A75373	2	603	3.6	113
493	regulatory factor	A35913	2	979	3.6	113
494	microtubule-associ	A53253	2	982	3.6	113
495	receptor protein k	T46033	2	1002	3.6	113
496	receptor protein k	T45647	2	1025	3.6	113
497	nuclear antigen EB	S27922	2	1069	3.6	113
498	neural plakophilin	T42209	2	1247	3.6	113
499	cell division prot	AF0611	2	1343	3.6	113
500	alpha-A-crystallin	I49477	2	2688	3.6	113
501	versican precursor	T42389	2	3381	3.6	113
502	mucin 1 precursor,	S10571	2	347	3.6	112.5
503	unknown protein T1	G96811	2	581	3.6	112.5
504	hypothetical prote	B86369	2	731	3.6	112.5
505	transcription fact	A57377	2	1075	3.6	112.5
506	internalin protein	AC1583	2	1237	3.6	112.5
507	hypothetical prote	T01367	2	1680	3.6	112.5
508	conserved hypothet	F87386	2	2479	3.6	112.5
509	probable tenascin	T09070	2	4006	3.6	112.5
510	glial growth facto	S32359	2	241	3.6	112
511	thyrotropin recept	T01787	2	252	3.6	112
512	thyrotropin recept	JC1319	1	253	3.6	112
513	probable pheromone	A41826	2	285	3.6	112
514	delta-like homeoti	S53716	2	383	3.6	112
515	transcription fact	S48756	2	413	3.6	112
516	serine/threonine k	AE2107	2	704	3.6	112
517	hypothetical prote	T04455	2	731	3.6	112
518	nuclear antigen EB	F84643	2	742	3.6	112
519	thyrotropin recept	QRHURH	1	764	3.6	112
520	brevican precursor	S49126	2	883	3.6	112
521	probable receptor-	G84652	2	960	3.6	112
522	probable receptor	T01784	2	990	3.6	112
523	hypothetical prote	T34433	2	1032	3.6	112
524	hypothetical prote	AB2217	2	1289	3.6	112
525	Ac0rf-91 protein -	D72861	2	224	3.6	111.5
526	gene BCRF2 protein	S32975	2	383	3.5	111.5
527	transcription fact	I41154	1	478	3.5	111.5
528	probable disease r	T05251	2	645	3.5	111.5
529	hypothetical prote	T46500	2	649	3.5	111.5
530	masquerade precurs	A55617	2	1047	3.5	111.5
531	disease resistance	T45787	2	1253	3.5	111.5
532	immediate-early pr	EDBE75	2	1298	3.5	111.5
533	restrictin precurs	JH0675	1	1353	3.5	111.5
534	hypothetical prote	T51023	2	2649	3.5	111.5
535	heart-restricted l	JC8063	2	274	3.5	111
536	hypothetical prote	H86459	2	478	3.5	111
537	probable disease r	T05260	2	509	3.5	111
538	PAC2 protein - yea	S50465	2	518	3.5	111
539	hypothetical prote	E70546	2	548	3.5	111
540	coagulation factor	S28941	2	603	3.5	111

Left listing:

541	3.5	111	S35049	2	610	mucin JBR57 - huma
542	3.5	111	T50150	2	620	yeast nrd1-like pr
543	3.5	111	QRHUUT	1	699	lutropin-choriogon
544	3.5	111	T17461	2	853	disease resistance
545	3.5	111	T21338	2	932	hypothetical prote
546	3.5	111	T48216	2	984	hypothetical prote
547	3.5	111	I38902	1	1721	retinoblastoma bin
548	3.5	111	A35844	2	2524	Xotch protein - Af
549	3.5	110.5	C55066	2	359	tyrosine decarboxy
550	3.5	110.5	A60058	2	421	neural cell adhesi
551	3.5	110.5	G86459	2	512	Hypothetical 55.6
552	3.5	110.5	A58674	1	525	neurotrophin-3 rec
553	3.5	110.5	T07970	2	533	aromatic-L-amino-a
554	3.5	110.5	JE0338	2	565	Frizzled-2 protein
555	3.5	110.5	T01267	2	684	leucine-rich repea
556	3.5	110.5	S35695	2	803	neurotrophin-3 rec
557	3.5	110.5	B56708	1	815	extracellular sign
558	3.5	110.5	T07015	2	855	Cf-4A protein - to
559	3.5	110.5	S33015	2	872	hypothetical prote
560	3.5	110.5	A31666	2	992	KIAA0641 protein.-
561	3.5	110.5	T00378	2	1207	glp1 protein precu
562	3.5	110.5	A32901	2	1295	rig-1 protein - mo
563	3.5	110.5	T14316	2	1344	polyketide synthas
564	3.5	110.5	T17412	2	1346	hypothetical prote
565	3.5	110.5	T00391	2	1736	hypothetical prote
566	3.5	110.5	T34022	2	2476	zonadhesin - pig
567	3.5	110	T51437	2	275	hypothetical prote
568	3.5	110	T04609	2	391	hypothetical prote
569	3.5	110	S32987	2	549	probable receptor-
570	3.5	110	D84889	2	691	hypothetical prote
571	3.5	110	D96711	2	708	protein kinase hom
572	3.5	110	T02154	2	719	thyrotropin recept
573	3.5	110	I48882	2	764	hypothetical prote
574	3.5	110	H70599	2	846	versican - pig-tai
575	3.5	110	T21700	2	846	apolipoprotein E r
576	3.5	110	A96770	2	951	probable potassium
577	3.5	110	D96756	2	1123	receptor-like prot
578	3.5	110	E86143	2	1483	F6F3.12 protein -
579	3.5	110	A55148	1	1711	protein-tyrosine-p
580	3.5	110	A24420	2	2703	notch protein - fr
581	3.5	110	T13049	2	2715	eyelid - fruit fly
582	3.5	110	T42730	2	3942	Basson protein -
583	3.5	109.5	A86228	2	213	hypothetical prote
584	3.5	109.5	T10361	2	279	hypothetical prote
585	3.5	109.5	T29479	2	318	hypothetical prote
586	3.5	109.5	E71415	2	428	probable coll wall
587	3.5	109.5	S36553	2	473	L2 protein - human
588	3.5	109.5	T44768	2	507	antifreeze glycope
589	3.5	109.5	S57459	2	538	hook-containing pr
590	3.5	109.5	JC5878	2	558	plasma hyaluronan-
591	3.5	109.5	S22544	2	583	transcription fact
592	3.5	109.5	I73633	2	612	gene trkC protein
593	3.5	109.5	A55178	2	825	neurotrophin recep
594	3.5	109.5	I73632	1	839	neurotrophin-3 rec
595	3.5	109.5	E97302	2	874	hypothetical prote
596	3.5	109.5	T21621	2	878	hypothetical prote
597	3.5	109.5	T19765	2	954	hypothetical prote
598	3.5	109.5	T47182	2	1299	genome polyprotein
599	3.5	109.5	RRWPYM	1	1776	proline-rich prote
600	3.5	109.5	T31070	2	2531	extensin-like prot
601	3.5	109.5	A34203	2	2717	DNA-binding protei
602	3.5	109	T05441	2	379	proline-rich prote
603	3.5	109	D85257	1	379	extensin-like prot
604	3.5	109	I52842	2	395	CD43 Lp-3 antigen
605	3.5	109	A43545	2	395	leukosialin CD43 -
606	3.5	109	S52796	2	403	prpL2 protein - hu
607	3.5	109	JQ1696	2	426	pistil extensin-li
608	3.5	109	T04868	2	431	hypothetical prote
609	3.5	109	A54595	2	437	transcription fact
610	3.5	109	C96756	2	598	receptor-like prot
611	3.5	109	T42671	2	613	hypothetical prote
612	3.5	109	S19087	2	833	gene Delta protein
613	3.5	109	T38236	2	1611	hypothetical prote

Right listing:

614	109	3.5	2809	2	T30213	G-cadherin - sea u
615	108.5	3.5	308	2	JC7125	epidermal growth f
616	108.5	3.5	389	2	S27200	proline-rich proce
617	108.5	3.5	402	2	A84581	probable disease r
618	108.5	3.5	418	2	T15142	hypothetical prote
619	108.5	3.5	499	2	AI1107	internalin B [impo
620	108.5	3.5	514	1	H70699	probable ppp prote
621	108.5	3.5	548	2	I37577	islet cell antigen
622	108.5	3.5	662	2	A45155	mucin FIM-C.1 - Af
623	108.5	3.5	698	2	I39713	celB protein - Agr
624	108.5	3.5	710	2	QQBE22	membrane antigen g
625	108.5	3.5	740	2	B84741	hypothetical prote
626	108.5	3.5	756	2	G86308	Similar to disease
627	108.5	3.5	764	2	A35956	thyrotropin recept
628	108.5	3.5	783	1	A38637	Ras interactor RIN
629	108.5	3.5	825	2	A40026	neurotrophin-3 rec
630	108.5	3.5	855	2	C82983	hypothetical prote
631	108.5	3.5	1011	2	C84524	probable disease r
632	108.5	3.5	1125	2	B41206	microtubule-associ
633	108.5	3.5	1176	2	T49482	hypothetical prote
634	108.5	3.5	1184	2	G01763	atrophin-1 - human
635	108.5	3.5	1344	1	A35175	mucin 1 precursor,
636	108.5	3.5	1357	2	T29265	hypothetical prote
637	108.5	3.5	1487	2	T02850	hypothetical prote
638	108.5	3.5	3707	2	S18252	heparan sulfate pr
639	108	3.4	348	2	JQ0431	hypothetical 35.5K
640	108	3.4	409	2	AG0752	flagellar hook-len
641	108	3.4	511	1	VGBE1K	glycoprotein C - h
642	108	3.4	542	2	I39540	chitinase (EC 3.2.
643	108	3.4	544	2	T17547	proline-rich proce
644	108	3.4	550	2	T36746	probable serine/th
645	108	3.4	638	1	XXAV	dihydrolipoamide S
646	108	3.4	741	2	T05250	probable disease r
647	108	3.4	862	2	S43922	versican - pig-tai
648	108	3.4	996	2	JE0237	apolipoprotein E r
649	108	3.4	1017	2	T31354	probable potassium
650	108	3.4	1217	2	T51140	disease resistance
651	108	3.4	1217	2	T51141	disease resistance
652	108	3.4	2783	1	A41948	alpha-fetoprotein
653	108	3.4	3511	2	A59295	unconventional myo
654	108	3.4	4613	2	T17409	polyketide synthas
655	108	3.4	7576	2	T17428	FK506 polyketide s
656	107.5	3.4	363	2	H87702	hypothetical prote
657	107.5	3.4	369	2	S20500	hydroxyproline-ric
658	107.5	3.4	414	2	C96770	hypothetical prote
659	107.5	3.4	427	2	S74211	PAS-6/7 protein pr
660	107.5	3.4	536	2	H71563	hypothetical prote
661	107.5	3.4	604	2	S25203	srmR protein - Str
662	107.5	3.4	655	2	G96524	protein TIN15.9 li
663	107.5	3.4	832	2	A31246	neurogenic protein
664	107.5	3.4	880	2	S00670	neurogenic repetit
665	107.5	3.4	881	2	B98320	cellulose synthase
666	107.5	3.4	1009	2	T45645	receptor kinase-li
667	107.5	3.4	1099	2	A56155	tumor suppressor p
668	107.5	3.4	1206	2	S24407	formin isoform IV
669	107.5	3.4	1324	2	S52863	DNA-binding protei
670	107.5	3.4	1468	2	S11515	formin - mouse
671	107.5	3.4	3534	1	T42567	tegument protein 2
672	107	3.4	176	2	A46606	platelet glycoprot
673	107	3.4	228	2	S53504	extensin-like prot
674	107	3.4	273	1	A28512	infected cell prot
675	107	3.4	354	2	A48931	transmembrane glyc
676	107	3.4	358	1	WMBE38	infected cell prot
677	107	3.4	416	1	SKXLAG	dermal gland prote
678	107	3.4	447	2	A39321	mucin - rat (fragm
679	107	3.4	452	2	C41602	transcription fact
680	107	3.4	518	2	F75460	hypothetical prote
681	107	3.4	615	1	KFHU12	coagulation factor
682	107	3.4	650	2	S59630	dystroglycan alpha
683	107	3.4	840	1	S69204	pheromone response
684	107	3.4	915	2	T12526	structural polypro
685	107	3.4	1063	1	GNWVR4	structural polypro
686	107	3.4	1376	2	G00043	osteonidogen - hum

No.		Score	ID		Len	Description
687	3.4	107	I58157	2	1389	periaxin - rat
688	3.4	107	T03221	2	2723	probable polyketid
689	3.4	106.5	T36248	2	7463	CDA peptide synthe
690	3.4	106.5	A32993	2	304	transcription fact
691	3.4	106.5	A41558	2	353	N-syndecan - rat (
692	3.4	106.5	B46629	2	505	mucin 6, gastric (
693	3.4	106.5	D86911	2	509	conserved hypothet
694	3.4	106.5	T10013	2	509	probable phosphopr
695	3.4	106.5	AD1570	2	517	internalin, probab
696	3.4	106.5	S06733	2	620	hydroxyproline-ric
697	3.4	106.5	AC2963	2	827	celB protein [impo
698	3.4	106.5	H96638	2	925	protein T1F9.20 [i
699	3.4	106.5	C75489	2	998	conserved hypothet
700	3.4	106.5	T13856	2	1003	ksr protein - frui
701	3.4	106.5	S57180	2	1161	probable membrane
702	3.4	106.5	S50832	2	1184	atrophin-1 - human
703	3.4	106.5	AB0168	2	1305	probable cell divi
704	3.4	106.5	T42607	2	1442	transcription acti
705	3.4	106.5	T18314	2	1892	hypothetical prote
706	3.4	106.5	S26058	2	2090	probable transform
707	3.4	106.5	S60254	2	2453	nuclear receptor c
708	3.4	106	T49996	2	135	AtAGP4 - Arabidops
709	3.4	106	A33532	2	167	mucin SMUC-40 - hu
710	3.4	106	I51920	2	216	mucin - rhesus mac
711	3.4	106	S65765	2	287	chitinase (EC 3.2.
712	3.4	106	S78691	2	405	flagellar hook-len
713	3.4	106	S47538	2	431	acrosin (EC 3.4.21
714	3.4	106	D41602	2	435	transcription fact
715	3.4	106	B39794	2	443	transcription fact
716	3.4	106	A24993	2	449	cellulase (EC 3.2.
717	3.4	106	A45977	2	567	Rab geranylgeranyl
718	3.4	106	B70803	2	666	hypothetical prote
719	3.4	106	D48613	2	701	gag polyprotein -
720	3.4	106	T01105	2	818	disease resistance
721	3.4	106	T51049	2	822	related to nucleol
722	3.4	106	S56015	2	850	gastric mucin MUC5
723	3.4	106	A49227	2	901	sialidase - Actino
724	3.4	106	T17233	2	914	hypothetical prote
725	3.4	106	A40136	2	1064	fibropellin Ia - s
726	3.4	106	A48613	2	1603	gag/pol polyprotei
727	3.4	106	B40505	2	1958	hypothetical prote
728	3.4	106	TVFF7L	1	2554	kinase-related pro
729	3.4	106	T42761	2	3938	Bassoon protein -
730	3.4	105.5	T01392	2	395	leucine-rich repea
731	3.4	105.5	A41537	2	486	DNA-binding protei
732	3.4	105.5	A42750	2	510	insulinoma-associa
733	3.4	105.5	T05257	2	668	probable disease r
734	3.4	105.5	T04568	2	688	protein kinase hom
735	3.4	105.5	S62400	2	695	amphiphysin (clone
736	3.4	105.5	T13078	2	772	KIAA0992 protein -
737	3.4	105.5	A48143	2	780	HF-1 regulatory el
738	3.4	105.5	S32954	2	952	hypothetical prote
739	3.4	105.5	A35098	2	1132	MHC class III hist
740	3.4	105.5	T00065	2	1172	hypothetical prote
741	3.4	105.5	T15264	2	1621	hypothetical prote
742	3.4	105.5	A38261	2	1712	masking protein pr
743	3.4	105.5	RRWPEM	1	1839	genome polyprotein
744	3.4	105.5	S14428	2	2477	fibronectin precur
745	3.4	105.5	JQ1303	1	3033	genome polyprotein
746	3.4	105.5	T05857	2	349	hypothetical prote
747	3.3	105	I37891	2	422	interleukin-11 rec
748	3.3	105	E75291	2	454	probable cell wall
749	3.3	105	T33110	2	460	hypothetical prote
750	3.3	105	A57601	2	486	transcription fact
751	3.3	105	VGBEF4	2	511	glycoprotein C - h
752	3.3	105	T34842	2	566	probable transfera
753	3.3	105	A70525	2	620	hypothetical prote
754	3.3	105	T08153	2	658	cysteine proteinas
755	3.3	105	JC1456	2	730	gelatinase B (EC 3
756	3.3	105	JC5643	2	764	thyroid stimulatin
757	3.3	105	A53800	1	847	mixed-lineage prot
758	3.3	105	I54343	2	895	dystroglycan - hum
759	3.3	105	A36355	2	976	protein-tyrosine k
760	3.3	105	A54164	2	1133	sterol regulatory
761	3.3	105	T30561	2	1135	Scythe protein - A
762	3.3	105	S57845	1	1136	protein-tyrosine k
763	3.3	105	T01397	2	1456	LTR gag/pol polypr
764	3.3	105	D75489	2	1658	hypothetical prote
765	3.3	105	S01956	2	1844	hypothetical prote
766	3.3	105	T30637	2	2133	hypothetical prote
767	3.3	105	A60979	2	2409	versican precursor
768	3.3	105	UIBO	1	2769	thyroglobulin prec
769	3.3	104.5	T17033	2	329	leucine rich repea
770	3.3	104.5	C70816	2	407	hypothetical prote
771	3.3	104.5	T35943	2	464	probable hydrolyti
772	3.3	104.5	T32812	2	530	hypothetical prote
773	3.3	104.5	G02919	2	639	transcription fact
774	3.3	104.5	T04856	2	662	hypothetical prote
775	3.3	104.5	A42395	2	700	lutropin receptor
776	3.3	104.5	A34458	1	707	gelatinase B (EC 3
777	3.3	104.5	A53796	2	707	gelatinase B (EC 3
778	3.3	104.5	T35192	2	744	probable ABC trans
779	3.3	104.5	T20950	2	755	hypothetical prote
780	3.3	104.5	QRXLL1	1	909	LDL receptor 1 pre
781	3.3	104.5	S28262	2	960	kinesin-related pr
782	3.3	104.5	JC4934	2	1117	delta-crystallin/E
783	3.3	104.5	E96624	2	1194	hypothetical prote
784	3.3	104.5	T37190	2	1241	nephrin - human
785	3.3	104.5	JC4851	2	1505	hypoxia-inducible
786	3.3	104.5	T19964	2	1851	hypothetical prote
787	3.3	104.5	S46216	2	1898	leukocyte antigen-
788	3.3	104.5	T36180	2	2117	CDA peptide synthe
789	3.3	104	A60095	1	232	larval glue protei
790	3.3	104	I49139	2	306	lymphotoxin-beta -
791	3.3	104	B64900	2	318	hypothetical prote
792	3.3	104	A46676	2	326	CD68 homolog macro
793	3.3	104	S43988	2	332	protein phosphatas
794	3.3	104	S68209	2	360	sds22 protein homo
795	3.3	104	A39481	2	365	serum response fac
796	3.3	104	D88103	2	426	protein W10G11.6 [
797	3.3	104	I49681	2	440	glyceraldehyde-3-p
798	3.3	104	S36536	1	470	L2 protein - human
799	3.3	104	A46611	2	537	myosin-binding pro
800	3.3	104	S65764	2	538	chitinase (EC 3.2.
801	3.3	104	S49525	2	593	glycoprotein G - s
802	3.3	104	I46031	2	712	gelatinase B (EC 3
803	3.3	104	S20582	2	895	dystrophin-associa
804	3.3	104	T24031	2	927	hypothetical prote
805	3.3	104	T16275	2	1045	hypothetical prote
806	3.3	104	T28657	2	1547	blackjack protein,
807	3.3	104	S68448	2	1575	synaptojanin, 170K
808	3.3	104	T31337	2	1711	1,4-beta-glucanase
809	3.3	104	A54970	2	1744	tensin, cardiac mu
810	3.3	104	T34513	2	3507	hypothetical prote
811	3.3	103.5	NBHUIB	1	206	platelet glycoprot
812	3.3	103.5	PQ0478	2	264	pistil extensin-li
813	3.3	103.5	D70845	2	281	hypothetical prote
814	3.3	103.5	PQ0479	2	393	pistil extensin-li
815	3.3	103.5	I55604	2	411	platelet glycoprot
816	3.3	103.5	T49292	2	419	hypothetical prote
817	3.3	103.5	A39794	1	444	regulatory protein
818	3.3	103.5	F75591	2	489	transcription fact
819	3.3	103.5	A26456	2	625	P49 secreted prote
820	3.3	103.5	T33044	2	654	hypothetical prote
821	3.3	103.5	F96637	2	889	hypothetical prote
822	3.3	103.5	T20123	2	889	hypothetical prote
823	3.3	103.5	T00353	2	968	hypothetical prote
824	3.3	103.5	I48974	1	975	receptor-protein t
825	3.3	103.5	S54986	2	980	regulatory protein
826	3.3	103.5	A29355	2	1020	fibronectin - chic
827	3.3	103.5	A54810	2	1144	TMV resistance pro
828	3.3	103.5	T35548	2	1171	hypothetical prote
829	3.3	103.5	T31420	2	1268	C-terminal domain-
830	3.3	103.5	B86398	2	1590	protein T7N9.24 [1
831	3.3	103.5	S23810	2	1603	collagen alpha 1(X
832	3.3	103.5	A42091	2	1638	transcription acti

Index	Score		Length	Accession	Count	Description
833	103.5	3.3	1733	B45344	1	probable nuclear a
834	103.5	3.3	3739	T17410	2	polyketide synthas
835	103	3.3	168	S52994	2	arabinogalactan-li
836	103	3.3	191	E84740	2	hypothetical prote
837	103	3.3	227	T27905	2	hypothetical prote
838	103	3.3	263	S01360	1	salivary glue prot
839	103	3.3	362	A44083	2	meq protein - Mare
840	103	3.3	367	AC1328	2	internalin protein
841	103	3.3	379	T16213	2	APX-1 protein homo
842	103	3.3	394	C84905	2	probable extensin
843	103	3.3	515	P70904	2	hypothetical prote
844	103	3.3	535	S76953	1	protein kinase (EC
845	103	3.3	550	G70597	2	probable proteinas
846	103	3.3	575	G70181	2	XllL2 protein - hu
847	103	3.3	611	B86387	2	unknown protein [i
848	103	3.3	648	F48613	2	hypothetical prote
849	103	3.3	701	JC7390	2	gag polyprotein -
850	103	3.3	793	TVRTTB	1	thyroid stimulatin
851	103	3.3	799	T04313	1	nerve growth facto
852	103	3.3	813	S67285	2	protein kinase Xa2
853	103	3.3	851	A55173	2	NUD1 protein - yea
854	103	3.3	863	S36327	2	cf-9 protein precu
855	103	3.3	915	T29092	2	clathrin assembly
856	103	3.3	1040	A82809	2	TSC-22 protein hom
857	103	3.3	1121	A40670	2	exodeoxyribonuclea
858	103	3.3	1199	G86441	2	nuclear envelope p
859	103	3.3	1201	T33369	2	unknown protein [i
860	103	3.3	1275	A39808	2	hypothetical prote
861	103	3.3	1340	T02831	2	proteoglycan core
862	103	3.3	1541	C54689	2	AAA protein L4171.
863	103	3.3	1894	GNNY5P	1	protein-tyrosine-p
864	103	3.3	2207	A43908	2	genome polyprotein
865	103	3.3	2481	S52093	2	fibronectin - Afri
866	103	3.3	3133	S01358	1	hemocytin - silkwo
867	102.5	3.3	217	T04739	2	salivary glue prot
868	102.5	3.3	252	T31880	2	hypothetical prote
869	102.5	3.3	316	I53043	2	hypothetical prote
870	102.5	3.3	338	S17313	2	transforming facto
871	102.5	3.3	352	F70555	2	transcription fact
872	102.5	3.3	371	S31719	2	hypothetical prote
873	102.5	3.3	379	B86272	2	proline-rich prote
874	102.5	3.3	383	S53718	2	protein F16A14.12
875	102.5	3.3	385	A54785	2	homeotic protein d
876	102.5	3.3	421	T30709	1	preadipocyte facto
877	102.5	3.3	507	A32385	2	core protein homol
878	102.5	3.3	627	D75393	2	erythropoietin rec
879	102.5	3.3	674	T05264	2	serine proteinase,
880	102.5	3.3	706	E30411	2	probable serine/th
881	102.5	3.3	730	I52580	2	synapsin Ia - bovi
882	102.5	3.3	760	S07896	1	gelatinase B (EC 3
883	102.5	3.3	904	T46170	1	transcription fact
884	102.5	3.3	907	E96636	2	disease resistance
885	102.5	3.3	942	JQ1674	2	hypothetical prote
886	102.5	3.3	964	JC5545	2	protein kinase TMK
887	102.5	3.3	1015	T46422	1	integrin beta-4 pr
888	102.5	3.3	1115	IJMSNL	1	neural cell adhesi
889	102.5	3.3	1223	T15316	2	hypothetical prote
890	102.5	3.3	1350	G36793	2	hypothetical prote
891	102.5	3.3	1367	S48478	2	glucan 1,4-alpha-g
892	102.5	3.3	1678	T35547	2	hypothetical prote
893	102.5	3.3	1779	T31085	2	xylanase - Caldice
894	102.5	3.3	1813	S46217	2	resistance protein
895	102.5	3.3	1863	A36429	2	protein-tyrosine-p
896	102.5	3.3	1875	S09553	2	integrin beta-4 ch
897	102.5	3.3	2207	JQ1663	2	genome polyprotein
898	102	3.3	301	S36779	2	hybrid proline-ric
899	102	3.3	307	A28996	2	ribosome-binding p
900	102	3.3	317	B36963	2	proline-rich prote
901	102	3.3	353	T49545	2	bcsA 5'-region pro
902	102	3.3	413	S74453	2	hypothetical prote
903	102	3.3	532	FQHUMP	1	hypothetical prote
904	102	3.3	554			macrophage colony-

Index	Description	Accession	Count	Length	Score	
906	Rab geranylgeranyl	JC5538	2	567	3.3	102
907	probable serine/th	B70747	1	585	3.3	102
908	protein B0207.1 [i	B87791	2	650	3.3	102
909	zinc finger protei	S22293	2	670	3.3	102
910	hypothetical proce	T12534	2	715	3.3	102
911	DELTA-like 1 - mou	I48324	2	722	3.3	102
912	hypothetical prote	D86278	2	728	3.3	102
913	probable receptor	E84846	2	890	3.3	102
914	cytokine receptor	A35782	1	896	3.3	102
915	progesterone recep	A39596	2	923	3.3	102
916	DNA binding protei	A55926	2	963	3.3	102
917	hypothetical prote	T04462	2	1008	3.3	102
918	hypothetical prote.	H75423	2	1021	3.3	102
919	serine/threonine p	D83637	2	1032	3.3	102
920	protein-tyrosine k	B49120	2	1052	3.3	102
921	hypothetical prote	D85383	2	1069	3.3	102
922	T20H2.9 protein -	A86335	2	1137	3.3	102
923	synGAP-b1 protein	T13958	2	1166	3.3	102
924	Ras-GTPase activat	T14270	2	1249	3.3	102
925	ras GTPase-activat	T14259	2	1293	3.3	102
926	adenylate cyclase	A33988	2	1692	3.3	102
927	hypothetical prote	S19151	2	1985	3.3	102
928	hypothetical prote	B84683	2	2218	3.3	102
929	transmembrane prot	S42612	2	2437	3.3	102
930	transcription coac	S39162	2	2440	3.3	102
931	CREB-binding prote	S39161	2	2441	3.3	102
932	collagen alpha 1(X	A40020	2	3124	3.3	102
933	cadherin-related t	IJFFTM	1	5147	3.2	102
934	mucin SAC (clone M	S53367	2	98	3.2	101.5
935	hypothetical prote	T47176	2	173	3.2	101.5
936	nonspecific cross-	A40428	2	244	3.2	101.5
937	hypothetical prote	T29359	2	372	3.2	101.5
938	yop targeted effec	T43599	2	409	3.2	101.5
939	nuclear pore compl	B56573	2	547	3.2	101.5
940	hypothetical prote	C87587	2	654	3.2	101.5
941	probable SF16 prot	B84869	2	657	3.2	101.5
942	hypothetical prote	T44753	2	710	3.2	101.5
943	C-Delta-1 - chicke	I50719	2	728	3.2	101.5
944	conserved hypothet	A87168	2	733	3.2	101.5
945	hypothetical prote	AF2089	2	833	3.2	101.5
946	transcription fact	A55384	2	869	3.2	101.5
947	collagen alpha 1(I	S40495	2	921	3.2	101.5
948	probable receptor-	G86420	2	947	3.2	101.5
949	seizure-related pr	I52657	2	977	3.2	101.5
950	protein-tyrosine k	A34076	1	984	3.2	101.5
951	serine proteinase	JC5569	2	1034	3.2	101.5
952	hypothetical prote	A85096	2	1039	3.2	101.5
953	homeotic protein 1	S06434	2	1429	3.2	101.5
954	sex comb protein -	T13748	2	1668	3.2	101.5
955	tensin - chicken	S27939	2	1733	3.2	101.5
956	alpha-2-macroglobu	A53102	1	4543	3.2	101.5
957	proline-rich prote	B24264	2	240	3.2	101
958	hypothetical prote	S72619	2	294	3.2	101
959	hypothetical prote	T34537	2	294	3.2	101
960	transcription fact	S25561	2	360	3.2	101
961	probable cell grow	A44478	2	373	3.2	101
962	engrailed homeodom	A48423	2	401	3.2	101
963	merozoite surface	A44997	2	482	3.2	101
964	probable penicilli	B86911	2	492	3.2	101
965	sensor histidine k	B87619	2	574	3.2	101
966	myosin-light-chain	A28798	2	610	3.2	101
967	dihydrolipoamide S	A40497	2	613	3.2	101
968	dihydrolipoamide S	XXHU	2	615	3.2	101
969	hypothetical 69K p	JQ0110	2	628	3.2	101
970	probable disease r	D84648	2	671	3.2	101
971	S-layer protein -	T18263	2	688	3.2	101
972	probable UvrD - My	D70951	2	700	3.2	101
973	transcription fact	I56187	2	739	3.2	101
974	hypothetical prote	T21602	2	796	3.2	101
975	HQRF1 protein - hu	QQBEC3	1	846	3.2	101
976	DNA-binding protei	A56037	2	1043	3.2	101
977	hypothetical prote	T32404	2	1127	3.2	101
978	neurocan precursor	S28764	2	1257	3.2	101

Index	Pct		Len	n	Accession	Description
979	101	3.2	1367	2	T33819	hypothetical prote
980	101	3.2	1513	2	A54895	mucin 2, intestina
981	101	3.2	1792	2	A57075	tensin - chicken (
982	101	3.2	2946	2	T15840	hypothetical prote
983	101	3.2	3176	2	CGHU3A	collagen alpha 3(v
984	100.5	3.2	138	2	D96715	protein F4N2.10 [i
985	100.5	3.2	262	2	T33408	hypothetical prote
986	100.5	3.2	262	2	B88400	protein H34I24.2 [
987	100.5	3.2	269	2	T26957	hypothetical prote
988	100.5	3.2	274	2	T46041	hypothetical prote
989	100.5	3.2	283	2	B88597	protein Y47D3B.6 [
990	100.5	3.2	314	2	T48514	hypothetical prote
991	100.5	3.2	384	2	T50921	carbamoyl-phosphat
992	100.5	3.2	401	2	S65138	glycoprotein antig
993	100.5	3.2	440	2	JC7807	Wiskott-Aldrich sy
994	100.5	3.2	504	2	AG2373	hypothetical prote
995	100.5	3.2	504	2	S56745	mucin (clone pGM31
996	100.5	3.2	512	2	E59437	F02569_2 protein [
997	100.5	3.2	597	2	JQ0107	zinc finger protei
998	100.5	3.2	677	2	T39713	hypothetical prote
999	100.5	3.2	798	2	T34248	homeotic protein C
1000	100.5	3.2	906	2	A43817	hypothetical prote
1001	100.5	3.2	975	2	S33121	protein ZC518.2 [i
1002	100.5	3.2	1024	2	T27631	transforming prote
1003	100.5	3.2	1030	2	H88859	hypothetical prote
1004	100.5	3.2	1106	1	TVHUGL	protein-tyrosine k
1005	100.5	3.2	1131	2	F96662	disease resistance
1006	100.5	3.2	1138	1	S24066	SEC31 protein - ye
1007	100.5	3.2	1220	2	T48928	spalt protein - mo
1008	100.5	3.2	1273	2	S58782	aggrecan - bovine
1009	100.5	3.2	1323	2	T30253	Xin protein - chic
1010	100.5	3.2	2327	2	T42630	chondroitin sulfat
1011	100.5	3.2	2562	2	T14266	apoprotein(a) (EC
1012	100.5	3.2	3562	2	A47171	neu differentiatio
1013	100.5	3.2	4548	1	S00657	hypothetical prote
1014	100	3.2	230	2	A56210	protein kinase C-b
1015	100	3.2	311	2	B86211	T-cell-specific tr
1016	100	3.2	334	2	G02409	yopM protein - Yer
1017	100	3.2	366	2	S61796	protein TPX-VT3 -
1018	100	3.2	367	2	A33950	serum response fac
1019	100	3.2	474	2	S15921	En/Spm-like transp
1020	100	3.2	476	2	C39481	hypothetical prote
1021	100	3.2	510	2	H84824	protein R19.6 [im
1022	100	3.2	535	2	T17212	probable PPE prote
1023	100	3.2	549	2	C87719	DNA ligase (EC 6.5
1024	100	3.2	556	2	D70940	polyadenylate-bind
1025	100	3.2	562	2	S75308	tetratricopeptide
1026	100	3.2	596	2	G75457	internalin protein
1027	100	3.2	628	2	S44138	hypothetical prote
1028	100	3.2	673	2	AF1143	hypothetical prote
1029	100	3.2	698	2	T51915	hypothetical prote
1030	100	3.2	698	2	T17261	probable cAMP-resp
1031	100	3.2	699	2	T09069	neuregulin-3 [impo
1032	100	3.2	713	2	T44447	leucine-rich repea
1033	100	3.2	725	2	T01268	hypothetical prote
1034	100	3.2	756	2	C87432	neuroendocrine-spe
1035	100	3.2	776	2	A46583	serine/threonine-s
1036	100	3.2	881	2	T01269	probable disease r
1037	100	3.2	1109	2	C84545	hairless protein -
1038	100	3.2	1161	2	T45294	resistance complex
1039	100	3.2	1182	2	I48378	probable cytoskele
1040	100	3.2	1240	2	T06404	EGF repeat transme
1041	100	3.2	1420	2	T37781	hypothetical prote
1042	100	3.2	1687	2	T30176	bacterial blight-r
1043	100	3.2	1791	2	T02345	leukocyte antigen-
1044	100	3.2	1802	2	T00020	peptide synthetase
1045	100	3.2	1897	2	TDHULK	cell wall protein
1046	100	3.2	2459	2	AF2136	pEARLI 1 protein h
1047	100	3.2	108	2	S08315	probable EGF-like
1048	99.5	3.2	177	2	T07642	Phox2 homeodomain
1049	99.5	3.2	230	2	A44074	hypothetical prote
1050	99.5	3.2	280	1	I48713	
1051	99.5	3.2	293	2	C75421	hypothetical prote

Index	Accession	n	Len		Pct	Description
1052	S05500	2	352	3.2	99.5	Ig alpha-1 chain C
1053	A1HU	1	353	3.2	99.5	Ig alpha-1 chain C
1054	S36438	1	353	3.2	99.5	BPPT protein - hyd
1055	TDHUM4	1	375	3.2	99.5	monocyte surface g
1056	VGBEKG	1	383	3.2	99.5	glycoprotein precu
1057	VGB175	2	387	3.2	99.5	Motch A protein -
1058	B48423	2	392	3.2	99.5	homeotic protein e
1059	VGBED2	1	393	3.2	99.5	glycoprotein D - h
1060	T46910	2	420	3.2	99.5	hypothetical prote
1061	JC4199	2	451	3.2	99.5	heat-shock protein
1062	C70986	1	476	3.2	99.5	probable serine/th
1063	F70699	2	491	3.2	99.5	probable pbpA prot
1064	S52215	2	530	3.2	99.5	hypothetical prote
1065	T28770	2	539	3.2	99.5	hypothetical prote
1066	T43952	2	647	3.2	99.5	hypothetical prote
1067	S62328	2	665	3.2	99.5	kinesin-like DNA b
1068	A86383	2	702	3.2	99.5	76.4K protein kina
1069	T24293	2	802	3.2	99.5	hypothetical prote
1070	AD1427	2	851	3.2	99.5	internalin, probab
1071	IJBONC	1	853	3.2	99.5	neural cell adhesi
1072	T35469	2	886	3.2	99.5	probable ATP /GTP-
1073	T19209	2	903	3.2	99.5	probable protein k
1074	T24294	2	949	3.2	99.5	hypothetical prote
1075	E82994	2	958	3.2	99.5	glycine cleavage s
1076	TSHUP4	1	961	3.2	99.5	thrombospondin 4 p
1077	T33470	2	1013	3.2	99.5	hypothetical prote
1078	T41720	2	1016	3.2	99.5	hypothetical prote
1079	A53767	2	1056	3.2	99.5	mucin MUC5B, trach
1080	T47424	2	1122	3.2	99.5	hypothetical prote
1081	T06403	2	1220	3.2	99.5	resistance complex
1082	T31353	2	1390	3.2	99.5	polyprotein - Arab
1083	T31422	2	1473	3.2	99.5	C-terminal domain-
1084	T17120	2	1742	3.2	99.5	cellulase (EC 3.2.
1085	A48205	2	3869	3.2	99.5	All-1 protein +GTE
1086	PQ0476	2	154	3.2	99	pistil extensin-li
1087	T09854	2	214	3.2	99	proline-rich cell
1088	GSFF3	1	307	3.2	99	salivary glue prot
1089	B41344	2	329	3.2	99	lutropin-choriogon
1090	D41344	2	329	3.2	99	lutropin-choriogon
1091	C41344	2	331	3.2	99	lutropin-choriogon
1092	T01296	2	358	3.2	99	leucine-rich repea
1093	A34170	1	415	3.2	99	acrosin (EC 3.4.21
1094	S45361	2	428	3.2	99	LRR47 protein - fr
1095	T34992	2	447	3.2	99	probable lipoprote
1096	T06416	2	466	3.2	99	cysteine proteinas
1097	AC0941	2	511	3.2	99	probable ABC trans
1098	S25128	2	543	3.2	99	61K protein - Auto
1099	I53106	2	564	3.2	99	gene gli protein -
1100	F75381	2	569	3.2	99	probable two-compo
1101	C75588	2	616	3.2	99	conserved hypothet
1102	T51383	2	638	3.2	99	receptor protein k
1103	C84726	2	641	3.2	99	probable receptor-
1104	F96542	2	686	3.2	99	probable protein k
1105	A41344	2	696	3.2	99	lutropin-choriogon
1106	S61239	2	701	3.2	99	hypothetical prote
1107	S30293	1	770	3.2	99	transcription fact
1108	JC7389	2	814	3.2	99	thyroid stimulatin
1109	C86203	2	860	3.2	99	hypothetical prote
1110	H86420	2	940	3.2	99	probable receptor-
1111	T19140	2	963	3.2	99	hypothetical prote
1112	C82630	2	1000	3.2	99	serine proteinase
1113	T49187	2	1097	3.2	99	hypothetical prote
1114	T42627	2	1147	3.2	99	ADP-ribosylation f
1115	T52348	2	1217	3.2	99	disease resistance
1116	T03748	2	1317	3.2	99	probable protein k
1117	T04426	2	1405	3.2	99	hypothetical prote
1118	A61262	2	1532	3.2	99	collagen alpha 1(X
1119	E70874	2	1538	3.2	99	probable ppsB prot
1120	S50065	2	1694	3.2	99	sialoadhesin - mou
1121	S44920	1	1799	3.2	99	ZK688.5 protein -
1122	TDFFLK	2	2029	3.2	99	protein-tyrosine-p
1123	E71436	2	2088	3.2	99	hypothetical prote
1124	T30283	2	6420	3.2	99	polyketide synthas

ID	%	ver	code	n	num	description
1125	98.5	3.1	T22763	2	230	hypothetical prote
1126	98.5	3.1	D88560	2	254	protein F58A4.1 [i
1127	98.5	3.1	I77461	2	342	luteinizing hormon
1128	98.5	3.1	T15422	2	349	hypothetical prote
1129	98.5	3.1	S50125	2	379	larval glue protei
1130	98.5	3.1	T18180	2	385	proline-rich prote
1131	98.5	3.1	S62335	2	393	I71-7 protein - fr
1132	98.5	3.1	A35005	1	434	u-plasminogen acti
1133	98.5	3.1	D72653	2	434	hypothetical prote
1134	98.5	3.1	B39481	2	464	serum response fac
1135	98.5	3.1	A44100	2	486	cell adhesion mole
1136	98.5	3.1	T47346	2	514	receptor protein k
1137	98.5	3.1	I77463	2	633	luteinizing hormon
1138	98.5	3.1	A49744	2	700	lutropin-choriogon
1139	98.5	3.1	A46302	2	707	PTB-associated spl
1140	98.5	3.1	T22808	2	770	hypothetical prote
1141	98.5	3.1	F59433	2	803	RhoGAP protein [im
1142	98.5	3.1	A42112	2	837	mucin-like peptide
1143	98.5	3.1	E88594	2	862	protein Y48A6B.11
1144	98.5	3.1	B86257	2	885	NBS/LRR disease re
1145	98.5	3.1	D86293	2	921	F7H2.22 protein -
1146	98.5	3.1	T26314	2	947	hypothetical prote
1147	98.5	3.1	T31100	2	1087	probable potassium
1148	98.5	3.1	T30248	2	1272	fragile X mental r
1149	98.5	3.1	T00346	1	1281	hypothetical prote
1150	98.5	3.1	T00078	1	1309	probable RNA-direc
1151	98.5	3.1	A44453	2	1396	translation initia
1152	98.5	3.1	B56101	2	1774	collagen alpha 1(X
1153	98.5	3.1	T29764	2	2180	hypothetical prote
1154	98.5	3.1	A42566	2	2339	omega-conotoxin-se
1155	98	3.1	T07641	2	182	pEARLI 1 protein h
1156	98	3.1	AF0123	2	291	probable antigenic
1157	98	3.1	A56943	2	296	sensory/motor neur
1158	98	3.1	S40973	2	303	hypothetical prote
1159	98	3.1	S09266	2	352	Ig alpha chain C r
1160	98	3.1	A42879	1	416	advanced glycosyla
1161	98	3.1	S50062	2	442	cell wall glycopro
1162	98	3.1	AI2449	2	499	hypothetical prote
1163	98	3.1	A56201	2	514	transcription fact
1164	98	3.1	S21961	2	534	proline-rich prote
1165	98	3.1	S65762	2	535	chitinase (EC 3.2.
1166	98	3.1	I68093	2	538	PRR2 delta - human
1167	98	3.1	A70836	2	538	hypothetical prote
1168	98	3.1	A42499	2	553	mullerian inhibiti
1169	98	3.1	WFHUM	1	560	mullerian inhibiti
1170	98	3.1	S48940	2	605	hypothetical prote
1171	98	3.1	S27962	2	614	modulator recognit
1172	98	3.1	C89243	2	631	protein F28C1.3 [i
1173	98	3.1	T21471	2	631	hypothetical prote
1174	98	3.1	S76492	2	715	lipoprotein nlpD -
1175	98	3.1	H59435	2	728	phosphoinositide-3
1176	98	3.1	T42614	2	750	probable envelope
1177	98	3.1	QQBEE3	1	788	HHLF1 protein - hu
1178	98	3.1	T43631	2	856	serine/threonine k
1179	98	3.1	C86257	2	889	resistance to Pseu
1180	98	3.1	S36326	2	896	clathrin assembly
1181	98	3.1	JC5526	2	1006	kinase-defective E
1182	98	3.1	T34101	2	1216	hypothetical prote
1183	98	3.1	T25933	2	1372	hypothetical prote
1184	98	3.1	H88380	2	1522	protein T22F7.3 [i
1185	98	3.1	A55645	2	1873	calcium channel, v
1186	98	3.1	S38480	2	2115	nonstructural prot
1187	98	3.1	T13828	2	3190	CREB-binding prote
1188	98	3.1	T08618	2	3623	intrinsic factor-B
1189	98	3.1	T10053	2	3635	laminin alpha 5 ch
1190	98	3.1	T22812	2	3871	hypothetical prote
1191	98	3.1	T17464	2	5069	rifamycin polyketi
1192	97.5	3.1	S55925	2	215	probable arabinoga
1193	97.5	3.1	A35037	1	266	insulin-like growt
1194	97.5	3.1	S71830	2	268	transcription coac
1195	97.5	3.1	A46241	2	277	interferon respons
1196	97.5	3.1	T09067	2	306	extensin-like prot
1197	97.5	3.1	TVMSFB	1	338	transforming prote
1198	97.5	3.1	S22395	2	362	fetuin precursor -
1199	97.5	3.1	JC4965	2	429	elk1 protein - mou
1200	97.5	3.1	T23087	2	460	hypothetical prote
1201	97.5	3.1	S22697	2	464	extensin - Volvox
1202	97.5	3.1	F83634	2	497	hypothetical prote
1203	97.5	3.1	T43282	2	511	alp21 protein - fi
1204	97.5	3.1	S54266	2	521	glycoprotein gC -
1205	97.5	3.1	B55066	2	531	tyrosine decarboxy
1206	97.5	3.1	A75594	2	563	ferredoxin-nitrite
1207	97.5	3.1	A48501	1	574	probable protein-1
1208	97.5	3.1	T41653	2	587	probable transcrip
1209	97.5	3.1	T33149	2	614	hypothetical prote
1210	97.5	3.1	B70754	2	626	probable serine/th
1211	97.5	3.1	JC6534	2	627	protein kinase 1 (
1212	97.5	3.1	AB0535	2	631	hypothetical prote
1213	97.5	3.1	A36749	2	662	transcription fact
1214	97.5	3.1	D40228	2	662	neurexin II-beta p
1215	97.5	3.1	EDBE23	1	676	immediate-early pr
1216	97.5	3.1	D96728	2	710	hypothetical prote
1217	97.5	3.1	AC2807	2	754	OmpA family protei
1218	97.5	3.1	B97586	2	754	hypothetical prote
1219	97.5	3.1	G02390	2	814	disintegrin-like m
1220	97.5	3.1	S51342	2	817	verprolin - yeast
1221	97.5	3.1	T17672	2	830	chitinase-like pro
1222	97.5	3.1	H96651	2	893	protein T3P18.19 [
1223	97.5	3.1	A54809	1	909	disease resistance
1224	97.5	3.1	AE0332	2	921	conserved hypothet
1225	97.5	3.1	T52517	2	929	hypothetical prote
1226	97.5	3.1	F87693	2	948	peptidase, M16 fam
1227	97.5	3.1	G86292	2	1006	hypothetical prote
1228	97.5	3.1	JC5765	2	1258	inositol polyphosp
1229	97.5	3.1	T51947	2	1392	probable transcrip
1230	97.5	3.1	C40228	2	1715	neurexin II-alpha
1231	97.5	3.1	JQ1555	1	1748	genome polyprotein
1232	97	3.1	F84522	2	191	probable proline-r
1233	97	3.1	T23867	2	238	hypothetical prote
1234	97	3.1	T26419	2	238	hypothetical prote
1235	97	3.1	T05717	2	330	probable extensin
1236	97	3.1	B26883	2	355	neural cell adhesi
1237	97	3.1	A39364	2	357	GDF-1 embryonic gr
1238	97	3.1	AE3003	2	379	conserved hypothet
1239	97	3.1	A86166	2	395	protein F21B7.6 [i
1240	97	3.1	T00914	1	397	leucine-rich repea
1241	97	3.1	A28172	2	421	spasmolysin precur
1242	97	3.1	S11674	2	428	acrosin (EC 3.4.21
1243	97	3.1	TVHUEK	1	428	transforming prote
1244	97	3.1	D98280	2	452	hypothetical 28.0K
1245	97	3.1	T35317	2	459	probable serine/th
1246	97	3.1	T02226	2	483	NBS-LRR type resis
1247	97	3.1	D97302	2	500	hypothetical prote
1248	97	3.1	G70904	2	530	hypothetical prote
1249	97	3.1	D89711	2	601	protein F40E10.4 [
1250	97	3.1	T22025	2	601	hypothetical prote
1251	97	3.1	TO2627	2	632	hypothetical prote
1252	97	3.1	FOFV1R	1	701	gag polyprotein -
1253	97	3.1	JC4566	2	860	chitinase (EC 3.2.
1254	97	3.1	D96662	2	966	hypothetical prote
1255	97	3.1	G96637	2	967	hypothetical prote
1256	97	3.1	A39962	2	1123	kinase-related tra
1257	97	3.1	T44438	2	1214	disease resistance
1258	97	3.1	A37967	1	1265	neural cell adhesi
1259	97	3.1	T35694	2	1690	ATP dependent DNA
1260	97	3.1	A54602	2	1734	microtubule-associ
1261	97	3.1	T00093	2	2055	hypothetical prote
1262	97	3.1	GNNY2W	1	2205	genome polyprotein
1263	97	3.1	T14119	2	3034	seven-pass transme
1264	96.5	3.1	S19129	2	346	proline-rich prote
1265	96.5	3.1	E75341	2	350	peptidyl-prolyl ci
1266	96.5	3.1	G70602	2	419	hypothetical prote
1267	96.5	3.1	I48755	2	430	mSAP1a - mouse
1268	96.5	3.1	B36389	2	444	transcription fact
1269	96.5	3.1	S22543	1	485	transcription fact
1270	96.5	3.1	F70765	2	487	hypothetical prote

SEQ	%	val	length	n	accession	description
1271	96.5	3.1	514	2	A31643	cell adhesion 80K
1272	96.5	3.1	528	2	B75310	conserved hypothet
1273	96.5	3.1	574	2	B35149	ipaH protein - Shi
1274	96.5	3.1	598	2	T42070	protein serine/thr
1275	96.5	3.1	635	2	F70874	probable membrane
1276	96.5	3.1	637	2	A75342	hypothetical prote
1277	96.5	3.1	646	2	T34532	hypothetical prote
1278	96.5	3.1	654	2	T45017	chemotaxis histidi
1279	96.5	3.1	669	2	T08827	hypothetical prote
1280	96.5	3.1	796	2	E96654	hypothetical prote
1281	96.5	3.1	825	1	EDBEXD	immediate-early pr
1282	96.5	3.1	1021	2	A86421	Receptor-like seri
1283	96.5	3.1	1209	2	T00373	hypothetical prote
1284	96.5	3.1	1241	2	T18311	hypothetical prote
1285	96.5	3.1	1557	2	T02859	probable serine/th
1286	96.5	3.1	2282	2	T42717	DNA-binding protei
1287	96.5	3.1	2352	2	T30201	Notch homolog prot
1288	96.5	3.1	26926	1	I38344	titin, cardiac mus
1289	96	3.1	214	2	T10737	extensin-like cell
1290	96	3.1	240	2	A24264	proline-rich prote
1291	96	3.1	287	2	C75494	cell division prot
1292	96	3.1	346	2	JA0159	cysteine proteinas
1293	96	3.1	445	2	T05887	hypothetical prote
1294	96	3.1	451	2	D88395	protein F53A3.6 [i
1295	96	3.1	483	2	S12741	transcription fact
1296	96	3.1	537	1	FOMVGV	gag polyprotein -
1297	96	3.1	580	2	T43481	probable mucin DKF
1298	96	3.1	594	2	S33561	ref(2)P protein -
1299	96	3.1	598	2	T48822	hypothetical prote
1300	96	3.1	635	1	WMBEW6	capsid protein - h
1301	96	3.1	858	1	IJRTNC	neural cell adhesi
1302	96	3.1	883	2	A96662	hypothetical prote
1303	96	3.1	907	2	AD2951	cell division prot
1304	96	3.1	910	2	H98331	McrB-related prote
1305	96	3.1	969	2	A75634	hypothetical prote
1306	96	3.1	1216	2	T26104	insulin receptor s
1307	96	3.1	1231	2	S30185	phosphoinositide-b
1308	96	3.1	1544	2	E59431	protein-tyrosine-p
1309	96	3.1	1615	2	B49502	MEGF8 protein - hu
1310	96	3.1	1737	2	T00209	protein-tyrosine-p
1311	96	3.1	1767	2	A49502	genome polyprotein
1312	96	3.1	1844	1	RRWPTM	transcription fact
1313	96	3.1	2529	2	A56923	zonadhesin - mouse
1314	96	3.1	5376	2	T42215	proline-rich prote
1315	95.5	3.1	188	2	D29149	conserved hypothet
1316	95.5	3.1	284	2	F95320	monocyte surface g
1317	95.5	3.0	366	1	TDMSM4	threonine synthase
1318	95.5	3.0	382	2	S75823	vasodilator-stimul
1319	95.5	3.0	384	2	S51796	hypothetical prote
1320	95.5	3.0	435	2	T46443	cellular hepatitis
1321	95.5	3.0	451	2	S71754	probable PE protei
1322	95.5	3.0	479	2	D70676	transcription fact
1323	95.5	3.0	486	2	AB2975	attK protein (U594
1324	95.5	3.0	486	2	A98308	myocyte-specific e
1325	95.5	3.0	501	2	S76563	hypothetical prote
1326	95.5	3.0	507	2	A46713	erythropoietin rec
1327	95.5	3.0	553	2	C75318	hypothetical prote
1328	95.5	3.0	570	2	A48836	fibropellin C prec
1329	95.5	3.0	571	2	T43456	hypothetical prote
1330	95.5	3.0	573	2	B70726	probable secD - My
1331	95.5	3.0	624	2	T49366	myocyte-specific e
1332	95.5	3.0	630	2	T31798	hypothetical prote
1333	95.5	3.0	650	2	S44806	F10E9.6 protein -
1334	95.5	3.0	685	2	C56591	E75 B steroid rece
1335	95.5	3.0	710	1	S70965	serine/threonine-s
1336	95.5	3.0	722	2	T22359	hypothetical prote
1337	95.5	3.0	749	2	E87599	hypothetical prote
1338	95.5	3.0	790	1	TVHUTT	nerve growth facto
1339	95.5	3.0	880	2	D89756	protein T23E7.2b [
1340	95.5	3.0	943	2	E84429	probable receptor-
1341	95.5	3.0	987	2	A54092	protein-tyrosine k
1342	95.5	3.0	1027	2	I38759	zinc finger/leucin
1343	95.5	3.0	1054	2	A30239	hydroxymethylgluta

SEQ	%	val	%	length	n	accession	description
1344	95.5	3.0	95.5	1159	2	I38465	probable potassium
1345	95.5	3.0	95.5	1255	2	T31065	diaphanous protein
1346	95.5	3.0	95.5	1256	2	T03096	CDO protein - rat
1347	95.5	3.0	95.5	1331	2	T49813	related to gastric
1348	95.5	3.0	95.5	1630	2	T00390	KIAA0614 protein -
1349	95.5	3.0	95.5	2761	2	T21064	hypothetical prote
1350	95	3.0	95	175	2	I38408	neu differentiatio
1351	95	3.0	95	227	2	C29149	proline-rich prote
1352	95	3.0	95	227	2	G70555	hypothetical prote
1353	95	3.0	95	239	2	S25618	hypothetical prote
1354	95	3.0	95	241	2	D43273	heregulin precurso
1355	95	3.0	95	273	2	C70551	hypothetical prote
1356	95	3.0	.95	326	2	A59232	ABA-responsive pro
1357	95	3.0	95	338	2	T06336	proline-rich prote
1358	95	3.0	95	385	1	I39498	GTP cyclohydrolase
1359	95	3.0	95	413	2	T52617	hypothetical prote
1360	95	3.0	95	477	2	S53362	mucin 5AC (clone J
1361	95	3.0	95	494	1	A29079	lymphocyte surface
1362	95	3.0	95	502	2	A55197	Wiskott-Aldrich sy
1363	95	3.0	95	636	2	I61718	neu differentiatio
1364	95	3.0	95	653	2	E84682	hypothetical prote
1365	95	3.0	95	662	2	I61722	neu differentiatio
1366	95	3.0	95	667	2	T17221	hypothetical prote
1367	95	3.0	95	673	2	T48012	hypothetical prote
1368	95	3.0	95	705	2	A35621	spore germination
1369	95	3.0	95	712	2	G02512	interleukin-1 rece
1370	95	3.0	95	760	2	T16726	hypothetical prote
1371	95	3.0	95	776	2	C96554	unknown protein [i
1372	95	3.0	95	799	2	T48889	serine/threonine p
1373	95	3.0	95	846	2	S52418	GTP-binding regula
1374	95	3.0	95	891	2	G84693	probable proline-r
1375	95	3.0	95	901	2	A44825	phosphoprotein, sy
1376	95	3.0	95	903	2	S60257	meltrin alpha - mo
1377	95	3.0	95	943	2	T34847	probable transcrip
1378	95	3.0	95	1024	2	S18251	collagen alpha 1(X
1379	95	3.0	95	1209	2	T13153	brahma associated
1380	95	3.0	95	1324	2	T14070	peptide synthetase
1381	95	3.0	95	1474	2	B85188	retrotransposon li
1382	95	3.0	95	1616	2	G70668	polyketide synthas
1383	95	3.0	95	1731	2	AB3045	ice nucleation pro
1384	95	3.0	95	1731	2	B98241	hypothetical prote
1385	95	3.0	95	1770	2	T18551	saframycin Mx1 syn
1386	95	3.0	95	1806	1	CGHU1B	collagen alpha 1(X
1387	95	3.0	95	2090	2	T30075	hypothetical prote
1388	95	3.0	95	2148	2	A56011	transcription fact
1389	95	3.0	95	2274	2	T30258	adenomatous polypo
1390	95	3.0	95	3084	1	MMMSA	laminin alpha-1 ch
1391	94.5	3.0	94.5	211	2	T03381	high sulfur zein p
1392	94.5	3.0	94.5	255	2	B75309	hypothetical prote
1393	94.5	3.0	94.5	255	2	S31096	proline-rich prote
1394	94.5	3.0	94.5	270	2	E87649	hypothetical prote
1395	94.5	3.0	94.5	277	2	I38857	microtubule-associ
1396	94.5	3.0	94.5	298	2	H87533	peptidase, M23/M37
1397	94.5	3.0	94.5	301	2	D87684	transcription regu
1398	94.5	3.0	94.5	358	2	A61188	probable transcrip
1399	94.5	3.0	94.5	376	2	H82988	hypothetical prote
1400	94.5	3.0	94.5	393	2	E82283	conserved hypothet
1401	94.5	3.0	94.5	464	2	A83557	probable amidase P
1402	94.5	3.0	94.5	569	2	T19128	hypothetical prote
1403	94.5	3.0	94.5	630	2	A39344	tumor-associated m
1404	94.5	3.0	94.5	665	2	E75461	probable cell wall
1405	94.5	3.0	94.5	708	2	JC4364	gelatinase B (EC 3
1406	94.5	3.0	94.5	719	2	T33170	hypothetical prote
1407	94.5	3.0	94.5	860	2	I48839	tenascin-X - mouse
1408	94.5	3.0	94.5	921	2	S42617	collagen alpha 1(I
1409	94.5	3.0	94.5	985	2	T06049	hypothetical prote
1410	94.5	3.0	94.5	1006	2	T00050	hypothetical prote
1411	94.5	3.0	94.5	1092	1	JN0635	neural cell adhesi
1412	94.5	3.0	94.5	1191	2	T13850	gene u-shaped prot
1413	94.5	3.0	94.5	1487	1	EDBEE1	immediate-early pr
1414	94.5	3.0	94.5	1690	1	CGHU1B	collagen alpha 4(I
1415	94.5	3.0	94.5	2062	1	G96602	probable receptor
1416	94.5	3.0	94.5	2302	2	T14328	protein-tyrosine-p

1417	94.5	3.0	FNHU	1	2386	fibronectin precur
1418	94.5	3.0	T26216	2	2484	hypothetical prote
1419	94.5	3.0	T26215	2	2607	hypothetical prote
1420	94	3.0	T02034	2	157	early light-induce
1421	94	3.0	S57346	2	263	interleukin 15 rec
1422	94	3.0	E72564	2	277	hypothetical prote
1423	94	3.0	T22919	2	293	hypothetical prote
1424	94	3.0	T10064	2	329	cytokinin-induced
1425	94	3.0	S28004	2	338	probable cell surf
1426	94	3.0	S76923	2	346	hypothetical prote
1427	94	3.0	A96826	2	356	T8K14.10 [imported
1428	94	3.0	T38309	2	421	probable cell wall
1429	94	3.0	A40492	2	456	early growth respo
1430	94	3.0	A36389	2	466	transcription fact
1431	94	3.0	B44997	2	476	merozoite surface
1432	94	3.0	S41819	2	522	nucleoporin p62 -
1433	94	3.0	C75286	2	559	hypothetical prote
1434	94	3.0	B36789	2	590	hypothetical prote
1435	94	3.0	I61719	2	639	neu differentiatio
1436	94	3.0	S50856	2	648	whn protein - rat
1437	94	3.0	JC7303	2	677	pectate lyase (EC
1438	94	3.0	A41090	1	693	serine/threonine-s
1439	94	3.0	S67265	2	791	hypothetical prote
1440	94	3.0	T36581	2	811	probable transmemb
1441	94	3.0	S51493	1	862	major nitrogen reg
1442	94	3.0	D70986	2	865	probable ABC trans
1443	94	3.0	A40091	1	878	interleukin-3 rece
1444	94	3.0	A40114	2	898	fasciclin II precu
1445	94	3.0	JC4361	2	918	scavenger receptor
1446	94	3.0	A48085	2	927	transcription fact
1447	94	3.0	C70876	2	939	hypothetical prote
1448	94	3.0	A70848	2	979	probable membrane
1449	94	3.0	G96606	2	1007	disease resistance
1450	94	3.0	G70868	2	1137	probable regulator
1451	94	3.0	E70977	2	1236	hypothetical prote
1452	94	3.0	JC5630	2	1320	TCOF1 protein - mo
1453	94	3.0	A48954	2	1331	mannan endo-1,4-be
1454	94	3.0	T18289	2	1335	racGAP protein - s
1455	94	3.0	T13720	2	1429	gene expanded prot
1456	94	3.0	T11974	2	1549	glutamate synthase
1457	94	3.0	T00080	2	1560	hypothetical prote
1458	94	3.0	T30074	2	2153	hypothetical prote
1459	93.5	3.0	D41132	2	172	collagen-related p
1460	93.5	3.0	T27610	2	278	hypothetical prote
1461	93.5	3.0	G70784	2	299	probable mmpS3 pro
1462	93.5	3.0	T46721	2	305	hypothetical prote
1463	93.5	3.0	T06482	2	352	probable cell wall
1464	93.5	3.0	S61924	2	362	cyst wall protein
1465	93.5	3.0	I50702	2	391	transcription fact
1466	93.5	3.0	B87335	2	458	hypothetical prote
1467	93.5	3.0	A35356	1	461	tumor necrosis fac
1468	93.5	3.0	AG1107	2	490	internalin G [impo
1469	93.5	3.0	T36501	2	522	probable serine/th
1470	93.5	3.0	A53437	2	530	poliovirus recepto
1471	93.5	3.0	T42100	2	556	serine/threonine p
1472	93.5	3.0	T18116	2	577	hypothetical prote
1473	93.5	3.0	T46005	2	662	receptor-like prot
1474	93.5	3.0	B75622	2	691	hypothetical prote
1475	93.5	3.0	T05840	2	718	subtilisin-like pr
1476	93.5	3.0	F96577	2	719	hypothetical prote
1477	93.5	3.0	A96574	2	854	protein F12M16.30
1478	93.5	3.0	QRXLL2	1	909	LDL receptor 2 pre
1479	93.5	3.0	F83257	2	919	hypothetical prote
1480	93.5	3.0	T35745	2	998	probable ATP-bindi
1481	93.5	3.0	JC7329	2	1121	WD-repeat protein
1482	93.5	3.0	B89066	2	2109	protein H05009.1 [
1483	93.5	3.0	T33247	2	2109	hypothetical prote
1484	93.5	3.0	T32497	2	2150	hypothetical prote
1485	93.5	3.0	C88369	2	2295	protein unc-52 [im
1486	93.5	3.0	T19821	2	3375	hypothetical prote
1487	93	3.0	T02262	2	209	high-methionine d-
1488	93	3.0	T07079	2	221	leucine-rich repea
1489	93	3.0	PC2022	2	235	mucin like protein
1490	93	3.0	328	2	S01359	salivary glue prot
1491	93	3.0	338	2	S38030	suppressor protein
1492	93	3.0	384	2	H70580	hypothetical prote
1493	93	3.0	413	2	AH2743	conserved hypothet
1494	93	3.0	416	2	G97524	hypothetical proce
1495	93	3.0	438	2	G87675	arylesterase-relat
1496	93	3.0	453	2	B42093	serum response fac
1497	93	3.0	465	2	B82515	alpha-L-fucosidae
1498	93	3.0	558	2	T50742	protoporphyrin IX
1499	93	3.0	560	1	JC4795	plasma hyaluronan-
1500	93	3.0	586	2	H86914	conserved hypothet

ALIGNMENTS

RESULT 1
JC5239
insulin-like growth factor acid-labile chain - baboon
C;Species: Papio sp. (baboon)
C;Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C;Accession: JC5239
R;Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like
A;Reference number: JC5239; MUID:97040714; PMID:8886027
A;Contents: liver
A;Accession: JC5239
A;Molecule type: mRNA
A;Residues: 1-605 <DEL>
A;Cross-references: UNIPARC:UPI000000D50E
C;Comment: This factor is structurally related to proinsulin and have insuline-like metal

Query Match   10.3%;   Score 322;   DB 2;   Length 605;
Best Local Similarity   36.2%;   Pred. No. 2e-11;
Matches 100;   Conservative 39;   Mismatches 97;   Indels 40;   Gaps 11;

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Qy    7 LLLPLLLL--LALG------PGVQG------CPSGCQCSQPQ----TVPCTARQGTT 45
                    |   |:|          ||::   :||||
Db    8 LALALLLLSWVALGPRSLEGAEPGTPGEAEGPACPATCACSYDDEVNELSVPCSSRNLTR 67

Qy   46 VPRDVPPDTVGLYVPENGITMLDASSFAGLPGLQLLDLSQNOIASLRLPRLLL------- 98
                |:|  |:|::  ||:  |:|:  :||  |:||:|
Db   68 LPDGIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGSLE-PQALLGLENLCH 126

Qy   99 LDLSHNSLLALEPGILDTANVEALRLAGLG---LQQLDEGLFSRLRNLHDLDVSDNQLER 155
                |:|: :||| |:||  |  |||:|| |||         |:| ||:|:|||:
Db  127 LHLERNQLRSLAVGTF--AYTPALALLGLSNNRLSRLEDGLFPEGLGNLWDLNLGWNSLAV 184

Qy  156 VP-PVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPR 214
                |:     :|:|||:|: ||:   ||
Db  185 LPDAAFRGLGGLRELVLAGN-RLAYLQPALFSGLAELRELDLSRNALRAIKANVFAQLPR 243

Qy  215 LRLLAAARNPFNCVCPLSWFG----PWVRESHVTLA 246
                |:|          ||: ||
Db  244 LQKLYLDRNLIAAVAPGAFLGLKALRWLDLSHNRVA 279
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RESULT 2
A41915
insulin-like growth factor-binding complex acid-labile chain precursor - human
N;Alternate names: Acid-Labile Subunit (ALS)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A41915
R;Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
Mol. Endocrinol. 6, 870-876, 1992
A;Title: Structure and functional expression of the acid-labile subunit of the insulin-li
A;Reference number: A41915; MUID:92357025; PMID:1379671
A;Accession: A41915
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-605 <LEO>

A;Cross-references: UNIPROT:P35858; UNIPARC:UPI000000088A; GB:M86826; NID:g184807; PIDN:
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:110171)
F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

Query Match　　　　　9.6%; Score 302; DB 2; Length 605;
Best Local Similarity　35.5%; Pred. No. 2.9e-10; Gaps 11;
Matches　98; Conservative　40; Mismatches　98; Indels 40;

Qy　　　7 LLLPLLLL--LALG--------PGVQG------CPSGCQCSQPQ----TVFCTARQGTT 45
　　　　　　 :||| ||||　　　　||||　　　　 :||::| 　||||||:
Db　　　8 LALALLLLSWVALGPRSLEGADPGTPGEAEGPACPAACVCSYDDDADELSVFCSSRNLTR 67

Qy　　 46 VPRDVPPDTVGLYVFENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLL-------- 98
　　　　　 :||||　||||　　||:|||||:||::| :|:||
Db　　 68 LPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLE-PQALLGLENLCH 126

Qy　　 99 LDLSHNSLLALEPGILDTANVEALRLAGLG---LQQLDEGLFSRLRNLHDLDVSDNQLBR 155
　　　　　 :| :|||||| 　||||　:||||||||:| |||::|
Db　　127 LHLERNQLRSLALGTF--AHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGWNSLAV 184

Qy　　156 VP-PVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPR 214
　　　　　 :|| ||||| ||||　:| :|　: :|| |||
Db　　185 LPDAAFRGLGSLRELVLAGN-RLAVLQPALFSGLAELRELDLSRNALRAIKANVFVQLPR 243

Qy　　215 LRLLAAARNPFNCVCPLSWFG----PWVRESHVTLA 246
　　　　　 || |||| |||　 |||
Db　　244 LQKLYLDRNLIAAVAPGAFLGLKALRWLDLSHNRVA 279

RESULT 3
NBHUIA
platelet glycoprotein Ib alpha chain precursor - human
N;Alternate names: membrane glycoprotein Ib alpha chain
N;Contains: glycocalicin
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A94174; A60435; A94173; A94174; I55355; I55355; PMID:3303030
R;Lopez, J.A.; Chung, D.W.; Fujikawa, K.; Hagen, F.S.; Papayannopoulou, T.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 5615-5619, 1987
A;Title: Cloning of the alpha-chain of human platelet glycoprotein Ib: a transmembrane p
A;Reference number: A94174; MUID:87289655; PMID:87289655
A;Accession: A94174
A;Molecule type: mRNA
A;Residues: 1-626 <LOP>
A;Cross-references: UNIPROT:P07359; UNIPARC:UPI000012B962; GB:J02940; NID:g183499; PIDN:
R;Wicki, A.N.; Walz, A.; Gerber-Huber, S.N.; Wenger, R.H.; Vornhagen, R.; Clemetson, K.J
Thromb. Haemost. 61, 448-453, 1989
A;Title: Isolation and characterization of human blood platelet mRNA and construction of
d cloning of a GPIb coding cDNA insert.
A;Reference number: A60435; MUID:90020160; PMID:2799758
A;Accession: A60435
A;Molecule type: mRNA
A;Residues: 207-467 <WIC>
A;Cross-references: UNIPARC:UPI0000174311

R;Titani, K.; Takio, K.; Handa, M.; Ruggeri, Z.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5614, 1987
A;Title: Amino acid sequence of the von Willebrand factor-binding domain of platelet mem
A;Reference number: A94173; MUID:87289654; PMID:3497398
A;Accession: A94173
A;Molecule type: protein
A;Residues: 17-315 <TIT>
A;Cross-references: UNIPARC:UPI0000174312
R;Hess, D.; Schaller, J.; Rickli, E.E.; Clemetson, K.J.
Eur. J. Biochem. 199, 389-393, 1991
A;Title: Identification of the disulphide bonds in human platelet glycocalicin.
A;Reference number: S16945; MUID:91301149; PMID:2070794
A;Accession: S16945
A;Status: preliminary
A;Molecule type: protein
A;Residues: 224-227;262-270;277-282 <HES>
A;Cross-references: UNIPARC:UPI0000174313; UNIPARC:UPI0000174314; UNIPARC:UPI0000174315
R;Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.
J. Biol. Chem. 267, 10055-10061, 1992
A;Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of ta
ations.
A;Reference number: I55355; MUID:92250564; PMID:1577776
A;Accession: I55355
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 412-427 <RES>
A;Cross-references: UNIPARC:UPI0000073621; GB:S34436; NID:g249176; PIDN:AAB22152.1; PID:
A;Note: variant D
C;Comment: Glycoprotein Ib (GPIb), a surface membrane protein of platelets, participates
C;Comment: Platelet activation apparently involves disruption of the macromolecular compl
C;Comment: Binding sites for von Willebrand factor and thrombin (the latter site with unk
C;Comment: Glycocalicin, which is approximately coextensive with the extracellular part o
C;Genetics:
A;Gene: GDB:GP1BA; GP1B
A;Cross-references: GDB:118806; OMIM:231200
C;Map position: 17per-17p12
C;Complex: heterodimer with platelet glycoprotein Ib beta chain (NBHUIB)
C;Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein re
C;Keywords: blood coagulation; duplication; glycoprotein; platelet membrane; tandem repea
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-626/Product: platelet glycoprotein Ib alpha chain #status predicted <MPT>
F;48-71/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;72-93/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;94-116/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;117-140/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;165-188/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;189-212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;379-430/Region: proline/threonine-rich 9-residue repeats
F;502-540/Domain: transmembrane #status predicted <TRM>
F;541-626/Domain: intracellular #status predicted <INT>
F;37,175/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;308/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match　　　　9.0%; Score 282; DB 1; Length 626;
Best Local Similarity　24.0%; Pred. No. 4.4e-09;
Matches　160; Conservative 72; Mismatches 244; Indels 190; Gaps 26;

Qy　　　9 LPLLLLALGPGVQGVQGCPSGCQCSQPQT---VFCTARQGTTVVPRDVPPDTVGLYVFEN--- 62
　　　　　 |||||||||||| | ||:||: :|
Db　　　1 MPLLLLLLLLPSPLHPHPICEVSKVASHLEVNCDKRNLTALPPDLPKDTTILHLSENLLy 60

Qy　　 63 ------GITMLDASSF------AGLPGLQLLDLSONQIASL-----RLPRLLL 98
　　　　　　 :||| |：|:
Db　　 61 TFSLATLMPYTRLTQLNLDRCELTKLQVDGTLPVLGTLDLSHNQLSLPLLGQTLPALTV 120

Qy　　 99 LDLSHNSLLALEPGIL-DTANVEALRLAGLQLGLQQLGNELKTLPGLLTPTKLEKLSLANNNLTELP 157
　　　　　 ||| ||| | :|| || |:|| ||: |
Db　　121 LDVSFNRLTSLPLGALRGLGELQELYIKGNLKTLPGLLIPTKLEKLSLANNNLTELP 180

Qy　　158 P-VIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSG--LFPR 214
　　　　　 | :||| | | | ::| |:
Db　　181 AGLLNGLENLDTLLQEN-----------SLYTIPKGFFGSHLLPF 215

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Qy   215 LRLLAAARNPFNCVCPLSWFGPWVRES----------HVTLASPEETRC------ 253
         |: |||||||||||||||| :|||:|            :||||| ||:|
Db   216 AFLHG---NPWLCNCEILYFRRWLQDNAENVYVWKQGVDVKAMTSNVASVQCDNSDKFPV 272

Qy   254 -HFPPKNAGRLLLE--LDYADFGCPATTTATVPTTRPVVREP-----------TA 295
          |:  |   |:||:  ||| || |
Db   273 YKYPGKGCPTLGDEGDTDLYDYYFPEDTEGDKVRATRTVVKFPTKAHTTPWGLFYSWSTA 332

Qy   296 LSSSLAPTWLSPTAPATE--------------------APSPPSTAPPTVGPV---PQ 330
         |:  | |: :|| |                        :|:||:| ||| ||    |
Db   333 SLDSQMPSSLHPTQESTKEQTTFPPRWTPNFTLHMESITFSKTPKSTTEPTPSPTTSEPV 392

Qy   331 PQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSSPTPVTPRPRSLT 390
          :  |:|| |:  |    |  ||  |||  ||   |||  | |:|:|||:||||||
Db   393 PEPAPNMTLEPTP--------SPTTPE---------PTSEPAPSPTTPEPTPIPT 431

Qy   391 LGIEP---VSPTSLRVGLQRVLQGSS--VQLRSLRLTYRNLSGPDKRLVTLR--LPASLA 443
         : :||   :| |:|  | :  | |:   | |:| | | :  |   :||  |:  ||:|
Db   432 IATSPTILVSATSLIITPKSTFLTTTKPVSLLESTKKTTIPELDQPPKLRGVLQGHLESSRN 491

Qy   444 EYTVTQLRPNATYSVCVMPLG----------------------PGRV-PEGBEACGEAHT 480
                |  || : | :  |                        ||:| |||:||| ||
Db   492 D---PFLHPD---FCCLLPLGFYVLGLFWLLFASVVLILLLSWVGHVKPQALDSGGQAAL 545

Qy   481 PPAVHSNHAPVTQAREGNLP--LLI----APALAAVLLAALAAVGAAYCVRRGRAMAAA 533
         |   ::| ||:|:|   ||:  |||    |||:|||||||||||||||| ||| |:|||
Db   546 TTATQTTHLELQRGRQVTVPRAWLLFLRGSLPTFRSSLFLWVRPNGRVGPLVAGRRPSAL 605

Qy   534 AQDKGQ 539
         :|  ||
Db   606 SQGRGQ 611

RESULT 4
JC1282
insulin-like growth factor-binding protein acid labile chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1282
R;Dai, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A;Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A;Reference number: JC1282; MUID:93038676; PMID:1384485
A;Accession: JC1282
A;Molecule type: mRNA
A;Residues: 1-603 <DAI>
A;Cross-references: UNIPROT:P35859; UNIPARC:UPI000125918; GB:S46785; NID:g258002; PIDN:
A;Experimental source: liver
A;Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match    9.0%;    Score 281.5;  DB 2;    Length 603;
Best Local Similarity    32.4%;   Pred. No. 4.5e-09;
Matches   92; Conservative  49; Mismatches 106; Indels  37; Gaps  11;

Qy     6 PLLLPLLLL-LALGP-GVQG-----------------CPSGGQCSQPQ----TVFCTARQGTT 45
         | :|| ||| :|||| |  |                 ||||:||| ||    :|||| : |
Db     8 PALVVLLAFWVALGPCHLQGTDPGASADAEGPQCPVACTCSHDDYTDELSVFCSSKNLTH 67

Qy    46 VPRDVPPDTVGLYVFENGITMLDASSFAGLPGLQLLDLSQNQIASLR-----LPRLLLL 99
         :| |:|  | ||::  |::| | |||| :|  | | |::| |:|||:     ||:|  |
Db    68 LPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALLGLQNLYYL 127

Qy   100 DLSHNSLLALEPGIL-DTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVP- 157
          | ||  |:| |||| |   ::|:|| ||||| |:|||| ||::| ||:::  |:|
Db   128 HLERNRLRNLAVGLFHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGWNSLVVLPD 187

Qy   158 PVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRL 217
          |: || ||: | ||| |  :|| | |  | |:|| |||:|  | | || :|||| |:|
Db   188 TVFQGLGNLHELVLAGN-KLTYLQPALFCGLGELRELDLSRNALRSVKANVFVHLPRLQK 246
```

```
Qy   218 LAAAARNPFNCVCPLSWFG----PWVRESHVTLAS-PEETRCHFP 256
         |  | ||| ||||||||     |||||||||:|| |||:||:|
Db   247 LYLDRNLITAVAPAGAFLGMKALRWLDLSHNRVAGLMEDT---FP 287

RESULT 5
JC6128
insulin-like growth factor binding complex acid labile chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: JC6128
R;Boisclair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T.
Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996
A;Title: Organization and chromosomal localization of the gene encoding the mouse acid la
A;Reference number: JC6128; MUID:96413591; PMID:8816745
A;Accession: JC6128
A;Molecule type: DNA
A;Residues: 1-603 <BOI>
A;Cross-references: UNIPROT:P70389; UNIPARC:UPI000000891; GB:U66900; NID:g1621612; PIDN
C;Comment: This protein is a serum protein and it is of the ternary complex in the physic
C;Genetics:
A;Gene: als
A;Map position: 17

Query Match    8.9%;    Score 278.5;  DB 2;    Length 603;
Best Local Similarity    32.8%;   Pred. No. 6.7e-09;
Matches   90; Conservative  48; Mismatches 101; Indels  35; Gaps  10;

Qy     6 PLLLPLLLL-LALGP-GVQG-----------------CPSGGQCSQPQ----TVFCTARQGTT 45
         | :|| ||| :|||| |  |                 ||||:||| ||    :||||| |
Db     8 PALVVLLAFWVALGPCVLQGTDPGASADAEGPQCPVTCTCSYDDYTDELSVFCSSRNLTQ 67

Qy    46 VPRDVPPDTVGLYVFENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLL-------- 98
         :| |:|  | ||::  |::| | |||| ::| | | |::| |:|:|:
Db    68 LPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWIRSLE-PQALLGLQNLYH 126

Qy    99 LDLSHNSLLALEPGIL-DTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVP 157
         |||||| ||||| ||| |: | ||| |||||| |::|:: |||| |:||||||||| |
Db   127 LHLERNLLRSLAAGLFHTPSLASLSLGNNLLGRLEEGLFRGLSHLWDLNLGWNSLVVLP 186

Qy   158 -PVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLR 216
           |: || ||: | ||| |  :|| | |  | |:|| |||:|  | | || :|||| |:
Db   187 DTVFQGLGNLHELVLAGN-KLTYLQPALLCGLGELRELDLSRNALRSVKANVFIHLPRLQ 245

Qy   217 LLAAARNPFNCVCPLSWFG----PWVRESHVTLA 246
          |  | ||| ||||||||     |||||||||:|
Db   246 KLYLDRNLITAVAPRAFLGMKALRWLDLSHNRVA 279

RESULT 6
T42218
slit-1 protein homolog - rat
N;Alternate names: MEGF4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42218
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs b
A;Reference number: 214126; MUID:98360089; PMID:9693030
A;Accession: T42218
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1531 <NAK>
A;Cross-references: UNIPROT:088279; UNIPARC:UPI000004F20B; EMBL:AB011530; NID:g3449289; I
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF4
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein re

Query Match    8.9%;    Score 278;  DB 2;    Length 1531;
Best Local Similarity    25.8%;   Pred. No. 2.1e-08;
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Matches 127; Conservative 56; Mismatches 207; Indels 102; Gaps 16;

```
Qy    6  PLLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGIT  65
            :||| |||::: |||:::|||||::
Db   16  PELWLLWAAAWRLGATACAPALCTCT-GTTVDCHGTGLQAIPKNIPRNTERLELNGNNIT  74

Qy   66  MLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGIL-DTANVEALRL  124
            :: ||||:|:|:| ||:  |::
Db   75  RIHKNDFAGLKQLRVLQLMENQIG-----------------AVERGAFPDMKELERLRL  116

Qy  125  AGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVP-PVIRGLTRLRLAGNTRIAQLRPE  183
Db  117  NRNQLQVLPELLFQNNQALSRLDLSENSLQAVPRKAFRGATDLKNLQLDKN-QISCIEEG  175

Qy  184  DLAGLAALQELDVSNLSLQALPGDLSGLFPPRLRLLAAAARNPFNCVCPLSWFGPWVRESHV  243
Db  176  APRALRGLEVLTLNNNNITTIPVSSFNHMPKLRTFRLHSNHLFCDCHLAWLSQWLRQ-RP  234

Qy  244  TLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPT  303
            |||                                         CTLSGSGCPA
Db  235  TIGL--FTQCSGPASLRGLNVAEVQKSEFSCSGQGEAAQVPA---------CTLSGSGCPA  284

Qy  304  WLSPTAPATEAPSPPSTAPPTVGPVPQPQ--------DCPPPSTCLNGGTCHLG------  348
Db  285  MCSCSNGIVDCRGKGLTAIPANLPETMTEIRLELNGIKSIPP---------GAFSPYR  333

Qy  349  ------TRHHLACLCPEGFGLYCESQMQGGTRPSPTPVTPRPPRSLTLGIEPVS--PT  399
Db  334  KLRRIDLSNNQIAEIAPDAFQGL------------RSLNSLVLYGNKITDLPR  374

Qy  400  SLRVGLQRYLQGSSVQLRSLRLTYRNLSGPD--KRLVTLRLPA------SLAEYTVTQL  450
            ||:                                         |||:||:
Db  375  GVFGGLY------TLQLLLNANKINCIRPDAFQDIQNLSLLSLYDNKIQSLAKGTFTSL  428

Qy  451  RPNATYSVCVMP  462
            || |:|:
Db  429  RAIQTLHLAQNP  440
```

RESULT 7
A53531
oncofetal trophoblast glycoprotein 5T4 precursor - human
N;Alternate names: oncofetal antigen 5T4
C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A53531; S40087
R;Myers, K.A.; Rahi-Saund, V.; Davison, M.D.; Young, J.A.; Cheater, A.J.; Stern, P.L.
J. Biol. Chem. 269, 9319-9324, 1994
A;Title: Isolation of a cDNA encoding 5T4 oncofetal trophoblast glycoprotein. An antigen
A;Reference number: A53531; MUID:94179356; PMID:8132670
A;Accession: A53531
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-420 <MEY>
A;Cross-references: UNIPROT:Q13641; UNIPARC:UPI000004CAD5; EMBL:Z29083; NID:g435654; PID
C;Keywords: duplication; glycoprotein; transmembrane protein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-420/Product: oncofetal trophoblast glycoprotein 5T4 #status predicted <MAT>

Query Match 8.4%; Score 264.5; DB 2; Length 420;
Best Local Similarity 28.1%; Pred. No. 2.9e-08;
Matches 103; Conservative 44; Mismatches 121; Indels 99; Gaps 15;

```
Qy    2  CSRVP-----LLLPLLLLLALG-------------------PGVQGCPS  26
            |||                                       PGVQGCPS
Db    5  CSRGPAAGDGRLRLARLALVLLGWVSSSSPTSSASFSSASAPFLASAVSAQPLPDQCPA  64

Qy   27  GCCQCSQ-PQTVFCTARQGTTVPRDVPPDTVGLYVFENGITMLDASSFAGLP---GLQLLD  82
            ||:|||                                              GLQLLD
Db   65  LCECSSAARTVKCVNRNLTEVPTDLPAYVRNLFLTGNQLAVLPAGAFARRPLAELAALN  124

Qy   83  LSQNQIASLR------LPRLLLLDLSHNSLLALEPGILDTANVEALRLAGLGLQQLDEGL  136
            ||:||                                    :: :|
Db  125  LSGSRLDEVRAGAFEHLPSLRQDLSHNPLADLSPFAFSGSNASV---------SAPSPL  175

Qy  137  FSRLRNLHDLDVSDNQLER-----VPPVI-RGLRGLTRLRLAGNTRIAQLRPEDLAGL  188
Db  176  VELILN-HIVPPEDERQNRSFEGMVVAALLAGRALQGLRRLELASN-HFLYLPRDVLAQL  233

Qy  189  AALQELDVSNLSLQALP---------------------GDLSGLFPPRLRLLAA  220
Db  234  PSLRHDLDLSNNSLVSLTVVSFRNLTHLESLHLEDNALKVLHNGTLAELQGL-PHIRVF-L  291

Qy  221  ARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGC----PA  276
Db  292  DNNPWVCDCHMADMVTWLKETEV-VQGKDRLTCAYPEKMRNRVLLELNSADLLDCDPILPP  350

Qy  277  TTTTATV  283
            : |:
Db  351  SLQTSYV  357
```

RESULT 8
T13953
MEGF5 protein - rat
N;Alternate names: slit protein homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13953
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs 1
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T13953
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1523 <NAK>
A;Cross-references: UNIPROT:O88280; UNIPARC:UPI00000E57A; EMBL:AB011531; NID:g3449291; 1
C;Genetics:
A;Gene: MEGF5
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r

Query Match 8.3%; Score 261; DB 2; Length 1523;
Best Local Similarity 26.3%; Pred. No. 2e-07;
Matches 93; Conservative 41; Mismatches 126; Indels 94; Gaps 14;

```
Qy   24  CPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGITMLDASSFAGLPGLQLLDL  83
            || | :|:| |||| ||: |::                    |:
Db  725  CPEQCTCVE-TVVRCSNRGLHTLPKGMPKDVTELYLEGNHLTAV-------------  767

Qy   84  SQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNL  143
            |:|                           :::||:::
Db  768  -PKELSTFR--QLTLIDLSNNS------------ISMLTNHTFSNMSHL  801

Qy  144  HDLDVSDNQLERVP-PVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQ  202
            |:|| ::| ||: |: |:| |||:|::                    :::|
Db  802  STLILSYNRLRCIPVHAFNGLRSLRVLTLHGN----------DISSVPEGSFNDLTSLS--  850

Qy  203  ALPGDLSGLFPPRLRLLAAAARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGR  262
            :|| |||||||:| |:|                              | | ||
Db  851  --------------HLALGINPLHCDCSLRWLSEWIKAGY--KEPGIARCSSPESMADR  893

Qy  263  LLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAP  322
            ||||                                          PCKNNGTCSQ
Db  894  LLLTTPTHRFQCKG--------PVDINIVAKCNACLSS--PCKNNGTCSQDPVEQYRCTCP  944

Qy  323  PTVGPVPQPQDC--PPSTCL----NGGTCHLGTRHH--LACLCPEGFTGLYCE  367
            ||:                     NGGTCHL        LACLCP GF GLYCE
Db  945  YSY----KGKDCTVPINTCVQNPCQHGGTCHLSBSHRDGFSCSCPLGFEGQRCE  994
```

RESULT 9
B36665
slit protein 2 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002

```
Qy    312 TEAPSPPSTAPPTVGPVPQP------------QDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
                |                          :||  ||:||||
Db    928 REYQC---------------LCQPGYHGKHCEFMIDACYNPCRNNATCTVLEEGRFSCQCAPG 976

Qy    361 FTGLYCESQM 370
              :|| ||:  ||
Db    977 YTGARCETNI 986


RESULT 10
A36665
slit protein 1 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
C;Accession: A36665; A31640; S13523
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and con
A;Reference number: A36665; MUID:91099665; PMID:2176636
A;Accession: A36665
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1480 <ROT>
A;Cross-references: UNIPARC:UPI0000150FD1; GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g86
R;Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
Cell 55, 1047-1059, 1988
A;Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of
A;Reference number: A31640; MUID:89077533; PMID:3144436
A;Accession: A31640
A;Molecule type: DNA
A;Residues: 881-1182,'G',1185-1404,'GT',1463-1464,'YHA' <RO2>
A;Cross-references: UNIPARC:UPI0000016BD7A; GB:M23543; NID:g340939; PID:g514357
C;Genetics:
A;Gene: FlyBase:sli
A;Introns: 1351/3
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein re
C;Keywords: alternative splicing; growth factor
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F;1028-1061/Domain: EGF homology <EGF>
F;1068-1099/Domain: EGF homology <EGF2>
F;1115-1148/Domain: EGF homology <EGF1>

Query Match        8.1%;  Score 255.5; DB 2;  Length 1469;
Best Local Similarity   21.4%; Pred. No. 3.9e-07;
Matches 105;  Conservative 52; Mismatches 168;  Indels 165;  Gaps 14;

Qy    24 CPSGCQCSQPQTVPCTARQGTTVPRDVP-------------------PDTVGLY 58
             || ||  || :||  :|| |||| :
Db   519 CPAMCHC-EGTTVDCTGRRLKEIPRDIPLHTTBELLLNDNELGRISSDGLFGRLPHLVKLE 577

Qy    59 VFENGITMLDASSFAGLPGLQLLDLSQNQIAS------LRLPRLLLDLSHNSLLALEPG 112
             :| | ::  :::|  | | |  :| |  :| |:| || | :|  |:
Db   578 LKRNQLTGISPNAFBGASHIQELQIGENKIKEISNKMFLGLHQLKTLNLLYDNQISCVMPG 637

Qy   113 ILDTAN-------------------VEALRLAGLGLQQLDEGLFSRLRNLHDLDV-- 148
                 :|                   || | |||::::::|:
Db   638 SFEHNSLTSLNLASNPFNCNCHLAWFAECVRKKSLNGGAARCGAPSKVRDVQIKDLPHS 697

Qy   149 ----------------------SDNQLERVP---PV------------------ 159
                                    ||: |
Db   698 EFKCSSENSBEGCLGDGYCPPSCTCTGTVVACSRNQLKEIPRGIPAETSBLYLESNEIEQI 757

Qy   160 ---IRGLRGLTRRLAGNTRIAQLRPEDLAGLAALQELDVS-------------NL 199
                |||||||  ||| |||  |||  ||||||| :
Db   758 HYERIRHLRSLTRLDLS-NNQITTLSNYTPANLTKLSTLIISYNKLQCLQRHALSGLNNL 816

Qy   200 SLQALPGDLSGLFPR---------LRLLAAARNPFNCVCPLSWFGPWVRBSHVTLASPEET 251
                :| :: || |           ::|:| :
Db   817 RVVSLHGNRISMLPEGSFEDLKSLTHIALGSNPLYCDCGLKWFSDWIKLDYV---EPGIA 873

Qy   252 RCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALUSSSLAPTWLSPTAPA 311
             :|:|: :| ||         ||:|:
Db   874 RCAEPEQMKDKLILSTPSSSFVCRGRVRNDILAKCNACFEQPCQNQAQCV------ALPQ 927
```

```
Qy    24 CPSGCQCSQPQTVFCTARQGTTVPRDVP--------------------PDTVGLY 58
         |||:||||||| ||:|||||||  ||||||          ||||||
Db   519 CPAMCHC-EGTTVDCTGRRLKEIPRDIPLHTTELLNDNELGRISSDGLFGRLPHLVKLE 577

Qy    59 VFENGITMLDASSFAGLPGLQLLDLSQNQIAS-----------LRLPRLLLDLSHNSLLALEPG 112
         ||||||||||||||||||||||||||||||           :||:|||:||||||||||||||
Db   578 LKRNQLTGIEPNAFEGASHIQELQLGENKIKEISNKMFLGIHQLKTLNLYDNQISCVMPG 637

Qy   113 ILDTAN-----------------VEALRLAGLGLQQLDEGLFSRLRNLHDLDV--- 148
         ||||||                 ||||:|||||||||||  |||:||||||||
Db   638 SFEHLNSLTSLNLASNPFNCNCHLAWFAECVRKKSLNGGAARCGAPSKVRDVQIKDLPHS 697

Qy   149 ----------------------SDNQLERVP---PV----------------- 159
                               ||||||||   ||
Db   698 EFKCSSENSEGCLGDGYCPPSCTCTGTVVACSRNQLKEIPRGIPAETSELYLESNEIEQI 757

Qy   160 ----IRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVS----------------NL 199
             |||||||||||||||||||||||||||||||||||||                 :||
Db   758 HYERIRHLRSLTRLDLIS-NNQITILSNYTFANLTKLSTLIISYNKLQCLQRHALSGLNNL 816

Qy   200 SLQALPGDLSGLFPR------------LRLLAAARNPFNCVCPLSWFGPWVRESHVTLASPEET 251
         |||||||||||||||            |||||||||||||||||||||||||||||||||||||
Db   817 RVVSLHGNRISMLPEGSFEDLKSLTHIALGSNPLYCDCGLKWFSDWIKLDYV--EPGIA 873

Qy   252 RCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPA 311
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   874 RCAEPEQMKDKLILSTPSSSFVCRGRVRNDILAKCNACFEQPCQNQAQCV------ALPQ 927

Qy   312 TEAPSPPSTAPPTVGPVPQP----------QDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
         |||||||||||||||||||          ||||||:||||||||||||||||||||||
Db   928 REYQC----------LCQPGYHGKHCEFMIDACYGNPCRNNATCTVLEEGRFSCQCAPG 976

Qy   361 FTGLYCESQM 370
         ||||||||||
Db   977 YTGARCETNI 986
```

RESULT 11

JC7973
synleurin - human
C;Species: Homo sapiens (man)
C;Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 15-Sep-2003
C;Accession: JC7973
R;Wang, W.; Yang, Y.; Li, L.; Shi, Y.
Biochem. Biophys. Res. Commun. 305, 981-988, 2003
A;Title: Synleurin, a novel leucine-rich repeat protein that increases the intensity of
e intensity of pleiotropic cytokine responses as an adhesion protein or a receptor.
A;Reference number: JC7973; PMID:12767927
A;Accession: JC7973
A;Molecule type: mRNA
A;Residues: 1-622 <WAN>
A;Cross-references: GB:AY280614
C;Comment: This protein that is a single span transmembrane leucine-rich repeat protein
C;Genetics:
A;Gene: slrn
A;Map position: 5q12.1
C;Keywords: cytokine; leucine-rich repeat; synleurin; transmembrane protein

```
Query Match            8.0%;    Score 251; DB 2; Length 622;
Best Local Similarity  23.1%;   Pred. No. 2.7e-07;
Matches 107;  Conservative 52;  Mismatches 142;  Indels 162;  Gaps 13;

Qy     2 CSRVPLLLPLLLLLALGPGVQGVQGPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFE 61
         |||:||:||||||||| |||||:||||||||||||||||||||||||||||||||||||||
Db    10 CLRLFIVVTCYLLLLLHKEILGCSSVCQLCTGRQINCRNLGLSSIPKNFPESTVFLYLTG 69

Qy    62 NGITMLDASSFAGLPGLQLLDLSQNQI-----ASLRLPRLLLDLSHNSLLALEPG--- 112
         ||||||||||||||||||||||||||     |:||||||:|||||||||||||||
Db    70 NNISYINESELTGLHSLVALYLDNSNILYYYPKAFVQLRHLYFLFLNNNFIKRLDPGIFK 129

Qy   113 ----------------ILDTAN 118
                         |||||
Db   130 GLLNLRNLYLQYNQVSFVPRGVFNDLIVSVQYLNLQRNRLTVLGSGTFVGMVALRIIDLSN 189
```

RESULT 12

NBHUA2
leucine-rich alpha-2-glycoprotein - human
C;Species: Homo sapiens (man)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 05-Dec-1998
C;Accession: A03211
R;Takahashi, N.; Takahashi, Y.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 1906-1910, 1985
A;Title: Periodicity of leucine and tandem repetition of a 24-amino acid segment in the
A;Reference number: A03211; MUID:85166241; PMID:3856868
A;Accession: A03211
A;Molecule type: protein
A;Residues: 1-312 <TAK>
A;Cross-references: UNIPARC:UPI00004EB47
C;Comment: The function of this plasma protein is not known.
C;Superfamily: leucine-rich alpha-2-glycoprotein; leucine-rich alpha-2-glycoprotein repe
C;Keywords: duplication; glycoprotein; plasma; tandem repeat
F;58-81/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;82-105/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;106-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;130-153/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;154-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;178-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;202-225/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;262-309/Domain: proteoglycan carboxyl-terminal homology <PCH>
F;2/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;8-21,268-294/Disulfide bonds: #status experimental
F;44,151,234,290/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;271/Binding site: carbohydrate (Asn) (covalent) #status absent

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Query Match            7.8%;    Score 243.5; DB 1; Length 312;
Best Local Similarity  27.5%;   Pred. No. 3.4e-07;
Matches 89;  Conservative 36;  Mismatches 94;  Indels 105;  Gaps 9;

Qy    25 PSGCQ---------CSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGITMLDASSFA 73
         |||||         |:|||||||||||||||||||||||||||||||||||||||||
Db     5 PKDCQVFRSDHGSSISCQPP------AEIPGYLPADTVHLAVEFFNLTHLPANLLQ 54

Qy    74 GLPGLQLLDLSQNQIASLR------LPRLLLDLSHNSLLALEPGI------LDTANVEA 121
         |||||||||||||||:          |||||||:||||||||||       |||||
Db    55 GASKLQELHLSSNGLESLSPEFLRPVPQLRVLDTRNALTGLPPGLFQASATLDTLVLKE 114

Qy   122 ---------------LRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPP-VIR 161
                        |||:|||||||||||||||:||||||||||| ||: ||||
Db   115 NQLEVLEVSWLHGLKALGHLDLSGNRLRKLPPGLLANFTLLRTLDLGGNQLETLPPDLLR 174

Qy   162 GLRGLTRLRLAGN------------------TRIAQLRPEDLAGLAALQELDVSN 198
         |||||||||||                    ::||:|||||||||||||||||
Db   175 GPLQLERLHLEGNKLQVLGKDLLPQDLRYLFLNGNKLARVAAGAFQGLRQLDMLDLSN 234
```

A;Gene: GDB:GP5
A;Cross-references: GDB:230236; OMIM:173511
A;Map position: 5per-5qter
C;Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane prote

Query Match   Best Local Similarity 7.7%; Score 240;   DB 2;   Length 560;
               Pred. No. 1e-06;
Matches 109;   Conservative 28; Mismatches 111; Indels 152; Gaps 14;

Qy   57 LYVFENGITMLDASSFAGLPGLQLLDLSQNQI----ASL-RLPRLLLLDLSHNSLLALE 110
Db 127 LFLDHNALRGIDQNMFQKLVNLQELAINQNQLDFLPASLFTNLENLKLLDLSGNNLTHLP 186

Qy 111 PGILDT-ANVEALRLAGLGLQQLDEGL----------------FSRLRNLHD 145
Db 187 KGLLGAQAKLERLLLHSNRIVSLDSGLLNSLGALTELQFHRNHIRSIAPGAFDRLPNLSS 246

Qy 146 LDVS-----------------DNQLERVPPVIRG------ 162
Db 247 LTLSRNHLAFLPSALFLHSNLTLTLTLFENPLAELPGVLFGEMGGLQELWLNRTQLRTLP 306

Qy 163 --LRGLTRLRLAGNT--RIAQLRPEDLAGLAALQELDV-- 196
Db 307 AAAFRNLSRLRYLGVTLSPRISALPQGAFQGLGEIQVLALHSNGLTALPDCLLRGLGKLR 366

Qy 197 ------------------SNLS-----------LQALPGDLSGLFPRLRLLAAARNPFNCV 228
Db 367 QVSLRRNRLRALPRALFRNLSSLESVQLDHNQLETLPGDVFGALPRLTEVLLGHNSWRCD 426

Qy 229 CPLSWFGPWVRESHVTLASPEE-TRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTR 287
Db 427 CGLGPFLGWLRQ-HLGLVGGEEPPRCAGPGAHAGLPLWALPGGDAECPG-----PRGP 478

Qy 288 PVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGP 327
Db 479 P--PRPAADSSS----------------EAPVHPALAPNSSEP 503

Qy 199 LSLQALPG-----------DLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRES 241
Db 235 NSLASVPEGLWASLGQPNWDMRDGFDISG-------NPWICDQNLSDLYRWLQAQ 282

Qy 242 HVTLASPEETRCHFPPKNAGRLLL 265
Db 283 KDKMFSQNDTRCAGPEAVKGQTLL 306

RESULT 13
A60164
platelet membrane glycoprotein V precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Jan-1993 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: A48030; A60164; A35483; B35483; C35483; A60432; A47507; S34329
R;Lanza, F.; Morales, M.; de La Salle, C.; Cazenave, J.P.; Clemetson, K.J.; Shimomura, T
J. Biol. Chem. 268, 20801-20807, 1993
A;Title: Cloning and characterization of the gene encoding the human platelet glycoprote
A;Reference number: A48030; MUID:94012616; PMID:8407908
A;Accession: A48030
A;Molecule type: DNA
A;Residues: 1-560 <LA2>
A;Cross-references: UNIPROT:P40197; UNIPARC:UPI000004B117; EMBL:Z23091; NID:g312501; PID
R;Shimomura, T.; Fujimura, K.; Maehama, S.; Takemoto, M.; Oda, K.; Fujimoto, T.; Oyama,
Blood 75, 2349-2356, 1990
A;Title: Rapid purification and characterization of human platelet glycoprotein V: the a
A;Reference number: A60164; MUID:90275263; PMID:2350580
A;Accession: A60164
A;Molecule type: protein
A;Residues: 365-384,'X',386-390,'X',392-395,'X',397,188-208,'I',210,27-50,'X',52-53,174-
,'XX',108,'T',61-72,'TK',75-77,'V',56-57,'G',479-487,'X',489-498,'X',500,'X',502-503,'X'
2FD; UNIPARC:UPI000017C2FE; UNIPARC:UPI000017C2F7; UNIPARC:UPI000017C300; UNIPARC:UPI000
R;Roth, G.J.; Church, T.A.; McMullen, B.A.; Williams, S.A.
Biochem. Biophys. Res. Commun. 170, 153-161, 1990
A;Title: Human platelet glycoprotein V: a surface leucine-rich glycoprotein related to a
A;Reference number: A35483; MUID:90321220; PMID:2372284
A;Accession: A35483
A;Molecule type: protein
A;Residues: 145-166,'I',168-169,'X',171-172 <ROT>
A;Cross-references: UNIPARC:UPI000017C303
A;Note: this proteolytic fragment was designated peptide M392
A;Accession: B35483
A;Molecule type: protein
A;Residues: 121-129,'W',131-135;466-468,'X',470 <RO2>
A;Cross-references: UNIPARC:UPI000017C304; UNIPARC:UPI000017C305
A;Note: this material was designated peptide M393 but may contain two peptides
A;Accession: C35483
A;Molecule type: protein
A;Residues: 252-266,'H',268-272,'X',274-279,'I',281-284,'I',286 <RO3>
A;Cross-references: UNIPARC:UPI000017C306
A;Note: this proteolytic fragment was designated peptide M401
R;Zafar, R.S.; Walz, D.A.
Thromb. Res. 53, 31-44, 1989
A;Title: Platelet membrane glycoprotein V: characterization of the thrombin-sensitive gl
A;Reference number: A60432; MUID:89163331; PMID:2922700
A;Accession: A60432
A;Molecule type: protein
A;Residues: 477-478,'FX',481-485,'E',487,'V',489-492,'V',495,'NQ',495,'E',497-498 <ZAF>
A;Cross-references: UNIPARC:UPI000017C307
R;Hickey, M.J.; Hagen, F.S.; Yagi, M.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 90, 8327-8331, 1993
A;Title: Human platelet membrane glycoprotein V: characterization of the polypeptide and the rela
A;Reference number: A47507; MUID:93391348; PMID:7690959
A;Accession: A47507
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-560 <RES>
A;Cross-references: UNIPARC:UPI000004B117; GB:L11238; NID:g388759; PIDN:AAA03069.1; PID
C;Comment: This platelet membrane protein is a substrate for thrombin.
C;Comment: The amino end of the intact protein is blocked.
C;Comment: This protein is absent in Bernard-Soulier syndrome.
C;Genetics:

RESULT 14
JC7763
neuronal leucine-rich repeat protein-3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: JC7763
R;Fukamachi, K.; Matsuoka, Y.; Kitanaka, C.; Kuchino, Y.; Tsuda, H.
Biochem. Biophys. Res. Commun. 287, 257-263, 2001
A;Title: Rat neuronal leucine-rich repeat protein-3: Cloning and regulation of the gene e
A;Reference number: JC7763; PMID:11549284
A;Contents: Fibrosarcoma cells
A;Accession: JC7763
A;Molecule type: mRNA
A;Residues: 1-707 <FUK>
A;Cross-references: UNIPROT:Q9ESY6; UNIPARC:UPI00004F0F2; GB:AF291437
C;Comment: This protein, a new member of the neuronal leucine-rich repeat protein family,
in protein-protein interaction and functions as a cell adhesion molecule or soluble ligar
C;Genetics:
A;Gene: nlrr-3
C;Keywords: cell adhesion

Query Match   Best Local Similarity 7.6%; Score 237;   DB 2;   Length 707;
               Pred. No. 2e-06;
Matches 127;   Conservative 80; Mismatches 222; Indels 186; Gaps 22;

Qy   6 PLLLPLLLLALGPGVQG--------CPSGCQCS--------QPQTVFCTARQGTTVP 47
Db   5 PLQIHVLLGLAITALVQAGDKKVDCPQLCTCEIRPWFTPRSIYMEASTVDCNDLGLLNFP 64

Qy   48 RDVPPDTVGLYVFENGITMLDASSFAGLP-GLQLLDLSQNQIASL------- 91
Db   65 ARLPADTQILLLQTNNIARIEHST--DFPVNLTGLDLSQNNLSSVTNINVQKMSQLLSVY 122

Qy   92 -------RLPRLLLLDLS---------HNSLLALEPGIL-- 114

```
Db  123  LEENKLTELPEKCLYGLSNLQELYVNHNLLSAISPGAFVGLHNLLRLHLNSNRLQMINSK  182

Qy  115  --DTANVEALRL------------AGLGLGQLDEGLFSRLRNLHDLD               147

Db  183  WFEALPNLEILMLGDNPILRIKDMNFQPLLKLRSLVIAGINLTEVPDDALVGLENLESIS  242

Qy  148  VSDNQLERVP------------PVIRGLRG                                165

Db  243  FYDNRLNKVPQVALQKAVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELVSIDS  302

Qy  166  -------LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQAL-PGDLSGLFPRLR   216

Db  303  LAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESL-PNLK  361

Qy  217  LLAAARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPA  276

Db  362  EISIHSNPIRCDCVIRWIN--MNKTNIRFMEPDSLFCVDPPEFGQQNVRQVHFRDM----  415

Qy  277  TTTTAVTVPTTRPVVREPTALSSSL---APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQD 333

Db  416  ------MEICLPLI-APESFPSILDVEADSYVSLHCRATAEPQ------PEIYWITPSGKR  463

Qy  334  CPPSTCLNGGTCHL-GTRHHLACLCPEGFTGLY---CESQMGQGTRPSPTPVTPRPPR--  387

Db  464  LLPNTLREKFYVHSEGTLDIRGITPKEG--GLYTCIATNIVGADLKSIMIKVGGFVPQDN  521

Qy  388  --SLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLABY  445

Db  522  NGSLNIKIRDIRANSVLVS--WKANSKILKSSVKWTAFVKTEDSQAAQSARIPSDVKVY   578

Qy  446  TVTQLRPNATYSVCV                                               460

Db  579  NLTHLKPSTEYKICI                                               593
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Db  338  ----EGAFNDLSA-----LSHLAIGANPLYCDCNMQWLSDWVKSEY---KEPGIARCAGPG 386

Qy  258  KNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAPSP   317

Db  387  EMADKLLLTTPSKKFTCQ----------GPMDITTQAKCNPCLSN                421

Qy  318  PSTAPPTVGPVP-----------QPQDCP------PSTCLNGGTCHL--GTRHHLACL    356

Db  422  PCKNDGTCNNDPVDFYRCTCPYGFKGQDCDVPIHACISNPCKHGGTCHLKEGENAGFWCT  481

Qy  357  CPEGFTGLYCE                                                  367

Db  482  CADGFEGENCE                                                  492


Search completed: January 28, 2007, 17:28:03
Job time : 71 secs
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RESULT 15

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T42626
secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)
N;Alternate names: neurogenic extracellular slit protein
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42626
R;Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.
Mech. Dev. 79, 57-72, 1998
A;Title: Distinct but overlapping expression patterns of two vertebrate slit homologs im
A;Reference number: Z22177; MUID:99279938; PMID:10349621
A;Accession: T42626
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1025 <HOL>
A;Cross-references: UNIPROT:Q9R1B9; UNIPARC:UPI00000BB104; EMBL:AF074960; NID:g4151258;
C;Genetics:
C;Gene: Slit2
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r

Query Match             7.4%;  Score 231;  DB 2;  Length 1025;
Best Local Similarity  24.0%;  Pred. No. 6.9e-06;
Matches   89;  Conservative  32;  Mismatches 122;  Indels 128;  Gaps 13;

Qy   24  CPSGCQCSQPQTVECTARQGTTVFRDVPPDTVGLYVFENGITMLDASSFAGLPGLQLLDL   83

Db  223  CPSECTCLD-TXVRCSNKGLKVLPKGIPKDVTELYLDGNQFTLV-PKELSNYKHLTLIDL  280

Qy   84  SQNQIASL------RLPRLLLDLSHNSLLALEPGILDTANVEALRLAGLGLGQQLDEGLF  137

Db  281  SNNRISTLSNQXFSNMTQLLJTLILSYNRLRCIPPRTFD----------GLKSL-----  323

Qy  138  SRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVS  197

Db  324  -RLLSLHGNDIS------VVP-----------------                       337

Qy  198  NLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPP  257
```